Figure 1

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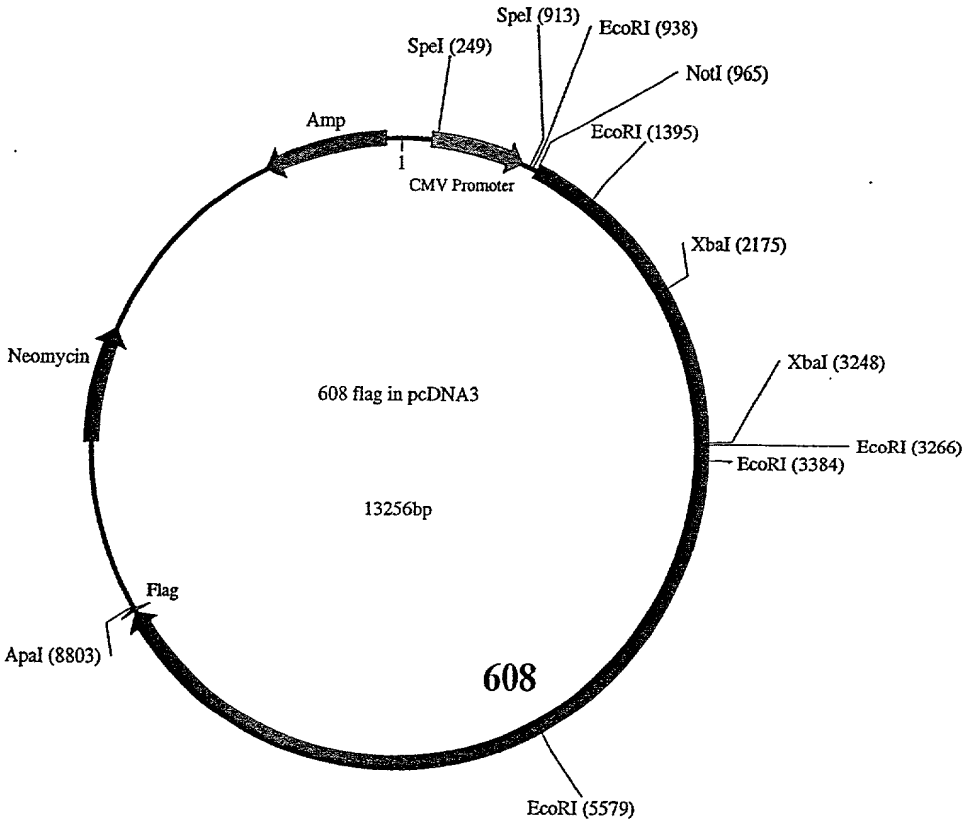
Figure 2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EcoRI (5579)

Figure 3

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Figure 4

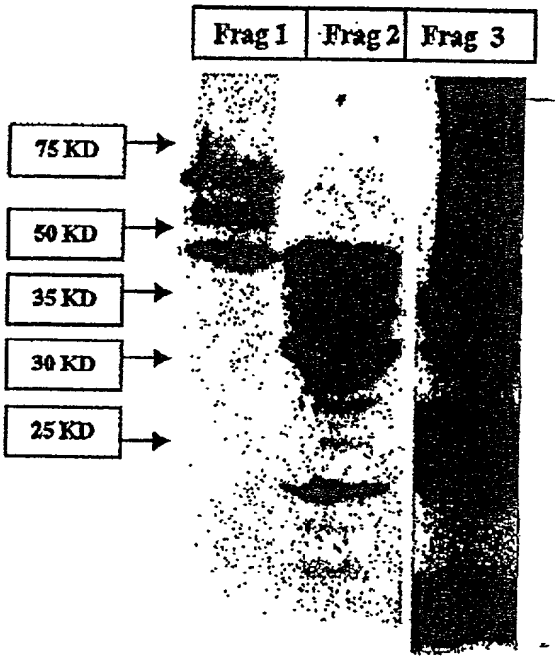


Figure 5

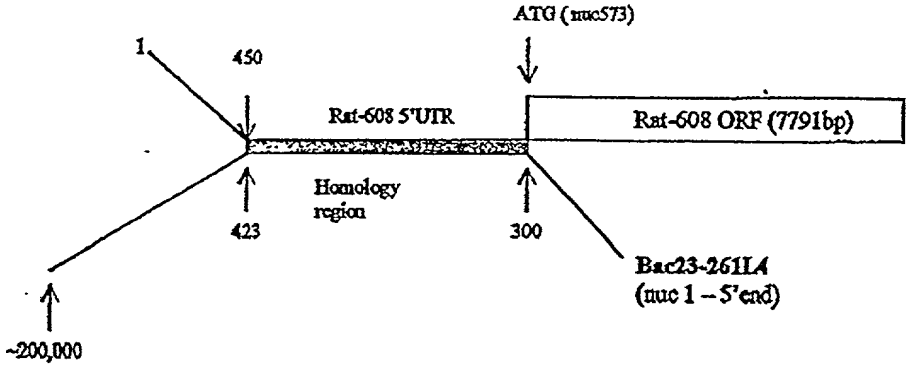
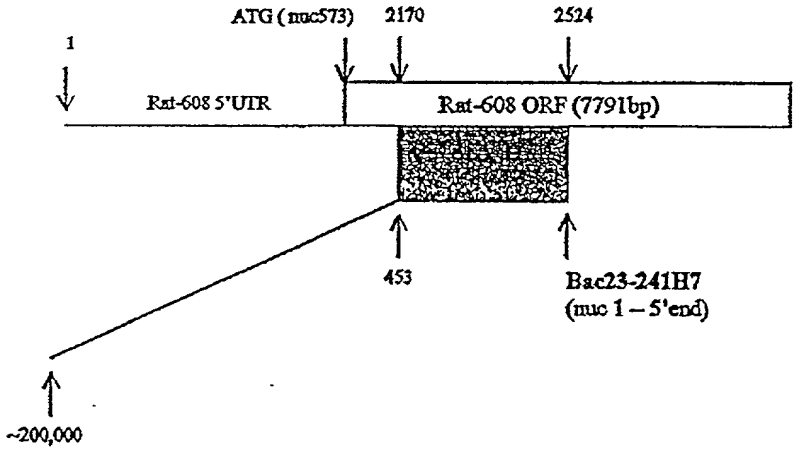


Figure 6



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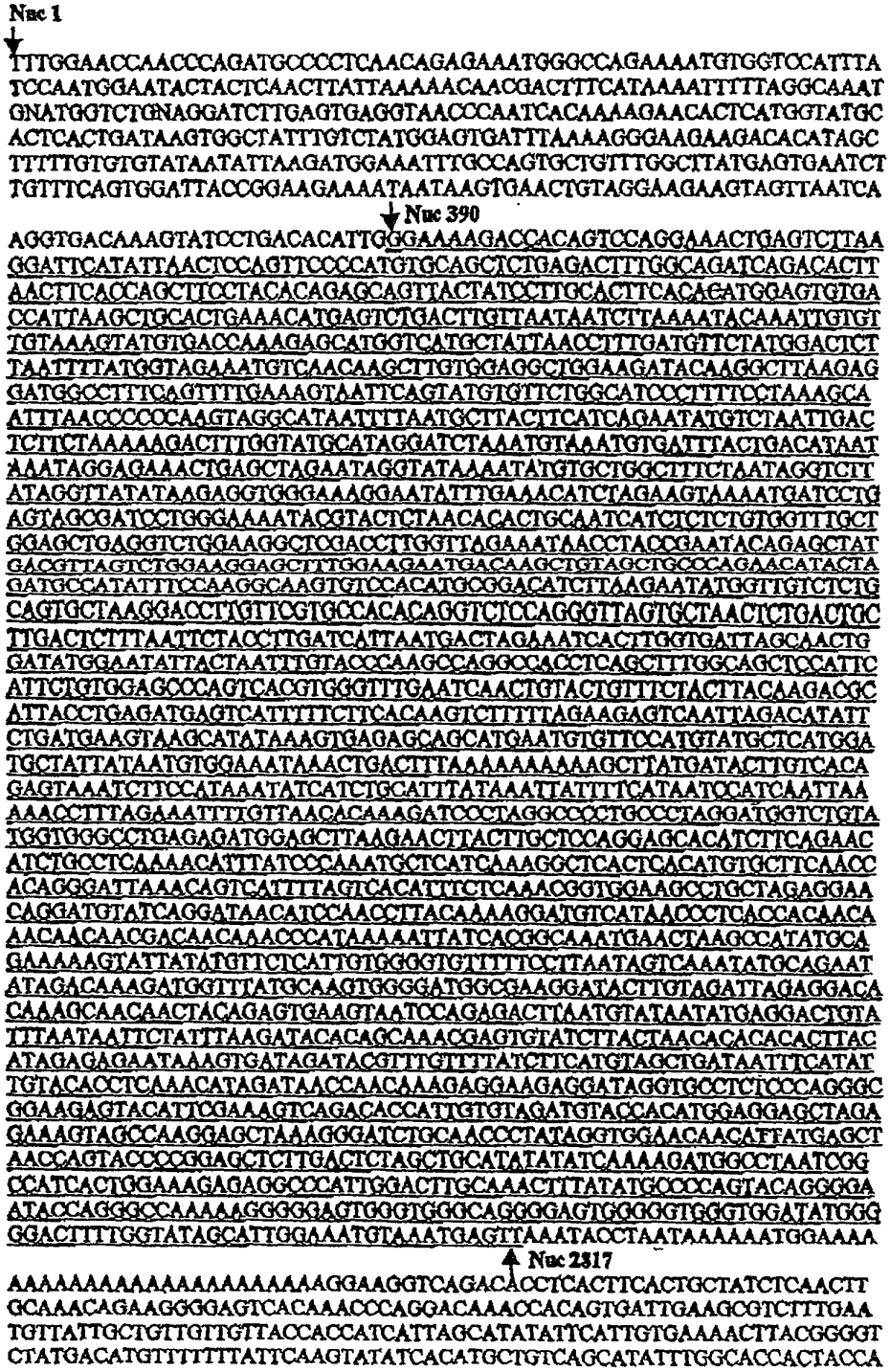

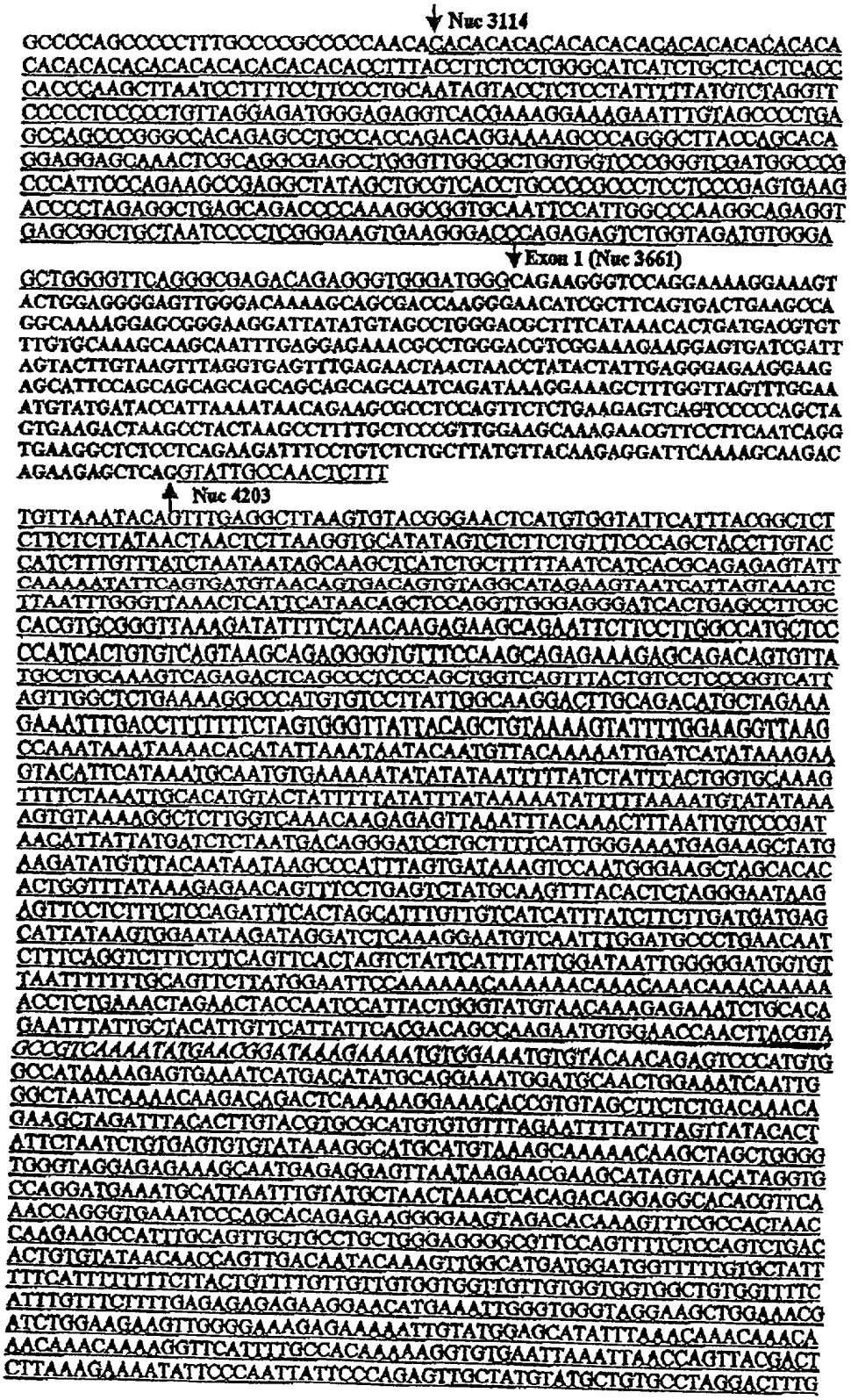
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Nuc 8218

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Exon 4 ? (Nuc 11286)

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Nuc 11680

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Nuc 11967

(SEQ ID NO:3)

Figure 8

Exon/Intron No.	Exon start	Exon end	Exon length	Intron length
1	1	542	542	2356
2	2898	3094	197	1334
3	4428	4557	130	3068
4	7625	8019	394	

Figure 9

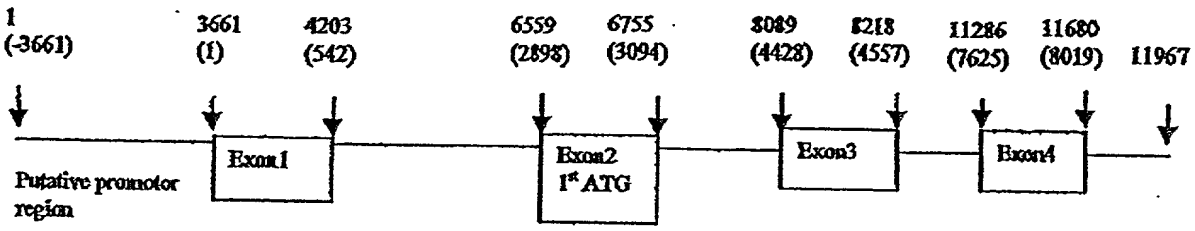
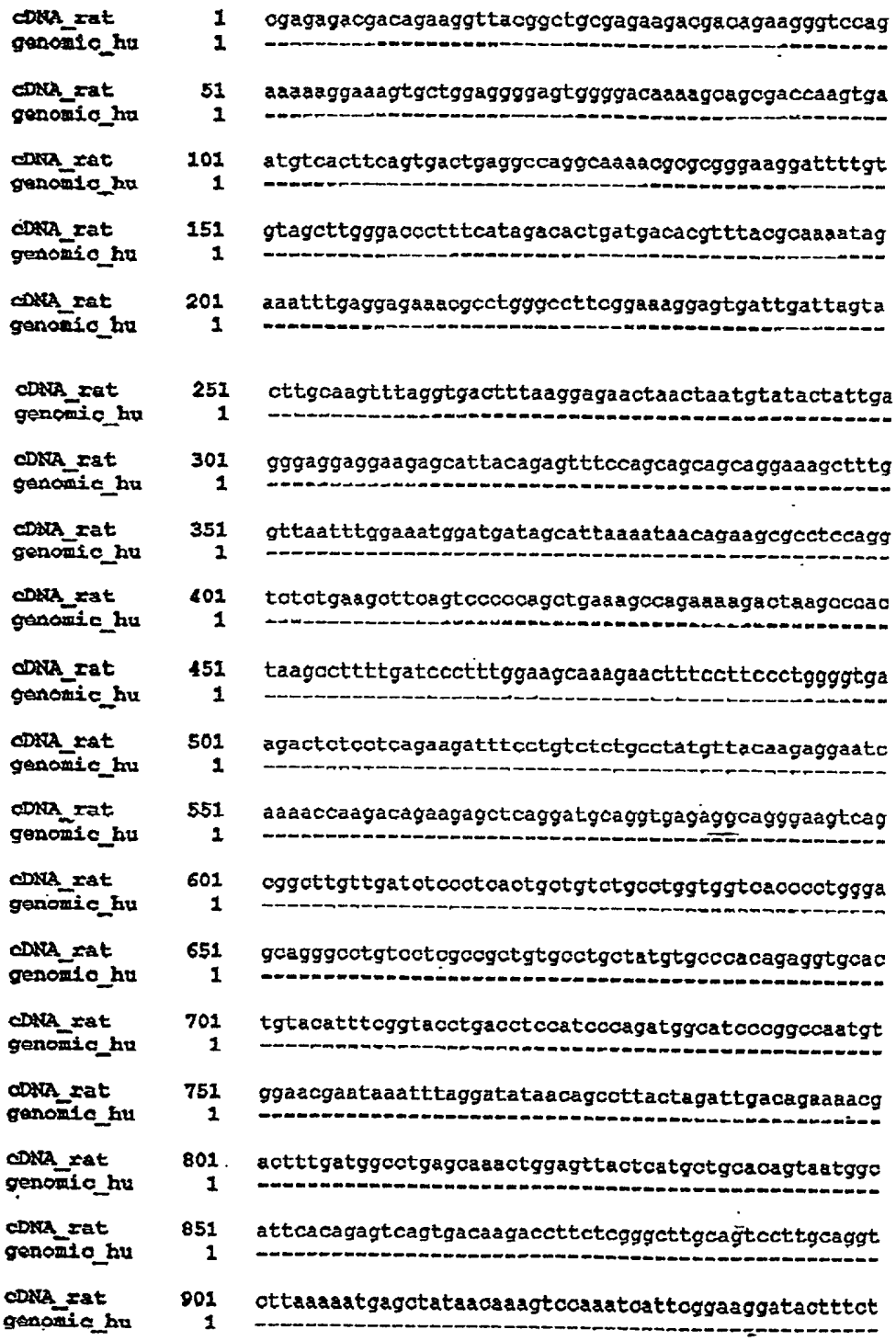


Figure 10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.c_hu	1590	gttcCAGTAATGATTGTAGCCTACCCTCCCCGAATTACAAAtcgtccACC
:at	8101	CAGGAACATGCTCAGGAGGACAGGGGAAGCCatgCAGCTCCACTGTGTGG
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Figure 11

Exon/Intron No.	Exon start	Exon end	Exon length	Intron length	Remarks
1	1	208	208	69	No valid splice site found upstream this exon
2	277	429	153	18	
3	447	485	39	1561	
4	2046	2244	199	1351	
5	3595	3724	130	3254	
6	6978	7359	382	4123	
7	11482	14903	3422	38	
8	14941	15307	367	51	
9	15358	15825	468	1039	
10	16864	~17760	~897	?	Last exon might be complete
11	?(1)	2317	~2317	25	Exon is not complete and start site is not known
12	2342	2397	56	-	

Figure 12

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Figure 13

A

Region						
General	Rat	Human	Region Length	% identity	% positives	% gaps
1-655	1-655	1-653	655	76	86	0
656-726	656-726	654-724	71	46	62	0
727-779	727-779	725-777	53	77	86	0
780-1634	780-1617	778-1612	655	38	53	4
1635-end	1618-end	1613-end	980	74	85	0
	Total	Alignment	2614	62	74	1

B

Region					
Rat	Mouse	Length	% identity	% positives	% gaps
1-238	1-238	238	91	92	1

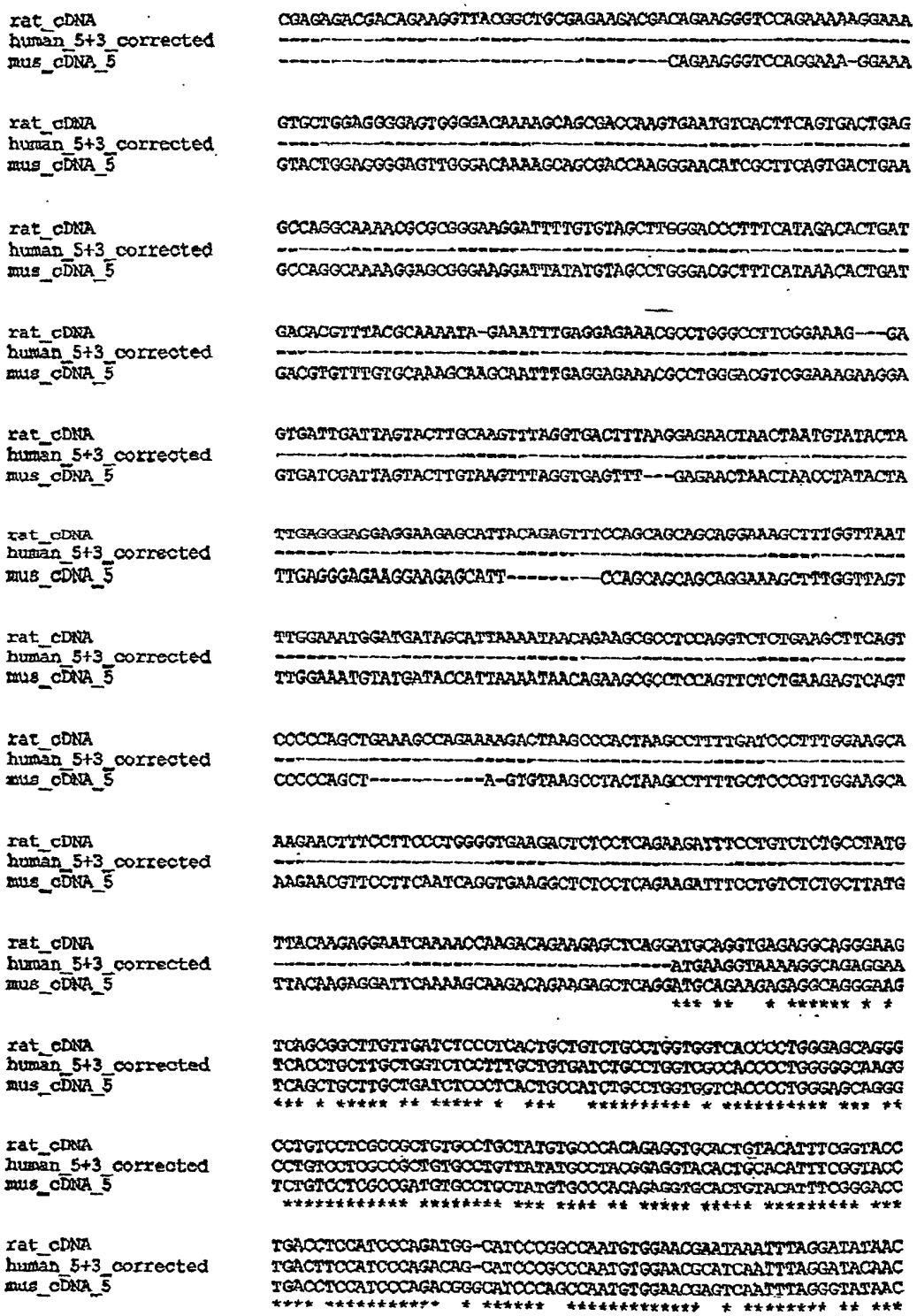
C

Region				
General	Rat	Human	Region Length	% identity
1-1965	1-1965	1-1965	1965	83
1966-2178	1966-2178	1966-2178	213	86
2179-2337	2179-2337	2179-2337	159	86
2338-4893	2338-4893	2338-4863	2565	63
4894-7833	4852-7791	4864-7761	2940	80
	Total	Alignment	7842	80

D

Region				
General	Rat	Mouse	Region Length	% identity
1-720	1-718	1-720	720	93

Figure 14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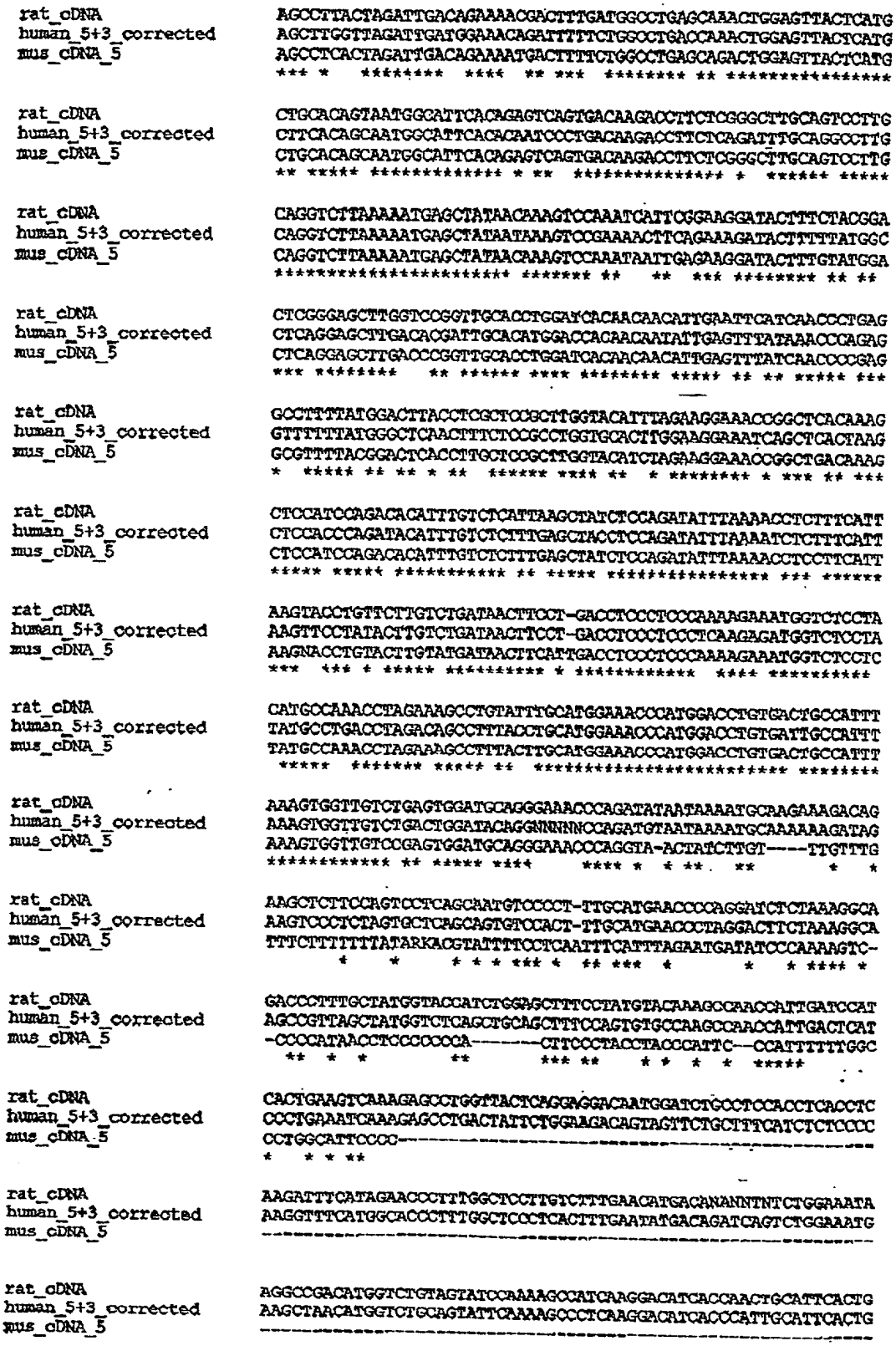
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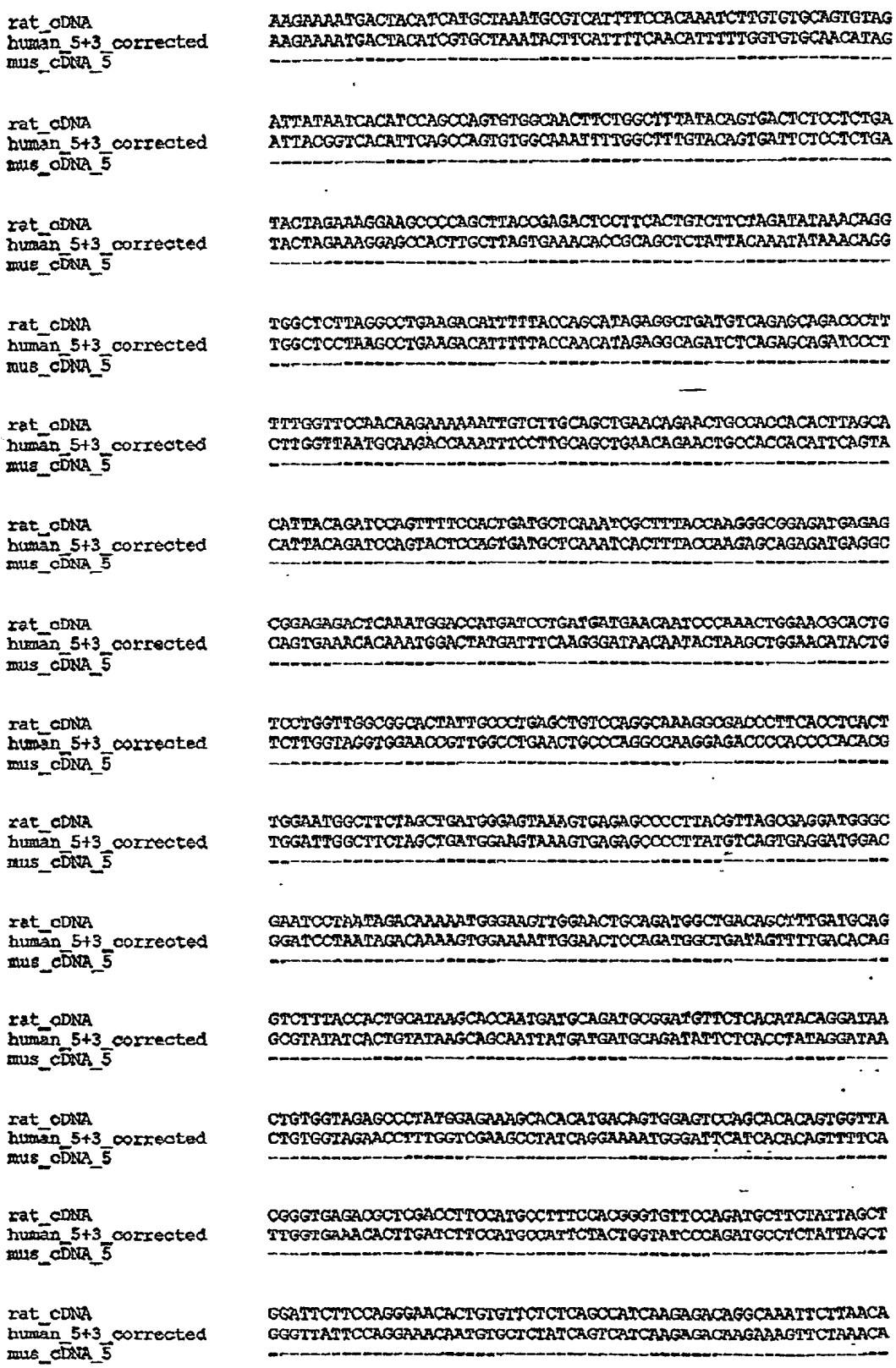
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mus_cDNA_5              ------------------------------------------------------------

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mus_cDNA_5              ------------------------------------------------------------

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human_5+3_corrected     TTGCTCATCTTAAGGAGCCACCAGGTGCACAACTCCGTACATCTGCTCTGATGGAGGCTG
mus_cDNA_5              ------------------------------------------------------------

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mus_cDNA_5              ------------------------------------------------------------

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mus_cDNA_5              ------------------------------------------------------------

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mus_cDNA_5              ------------------------------------------------------------

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mus_cDNA_5              ------------------------------------------------------------

rat_cDNA                CAGCTGTGACAAAGAGTATGAACCCATCCATAGCAAGCAAAATAGAAGATACAACCAACC
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mus_cDNA_5              ------------------------------------------------------------

rat_cDNA                AAAACCCAATCATTATCTTTCCATC---------AGTAGCTGAAATTCGAGATTCTG-CT
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mus_cDNA_5              ------------------------------------------------------------
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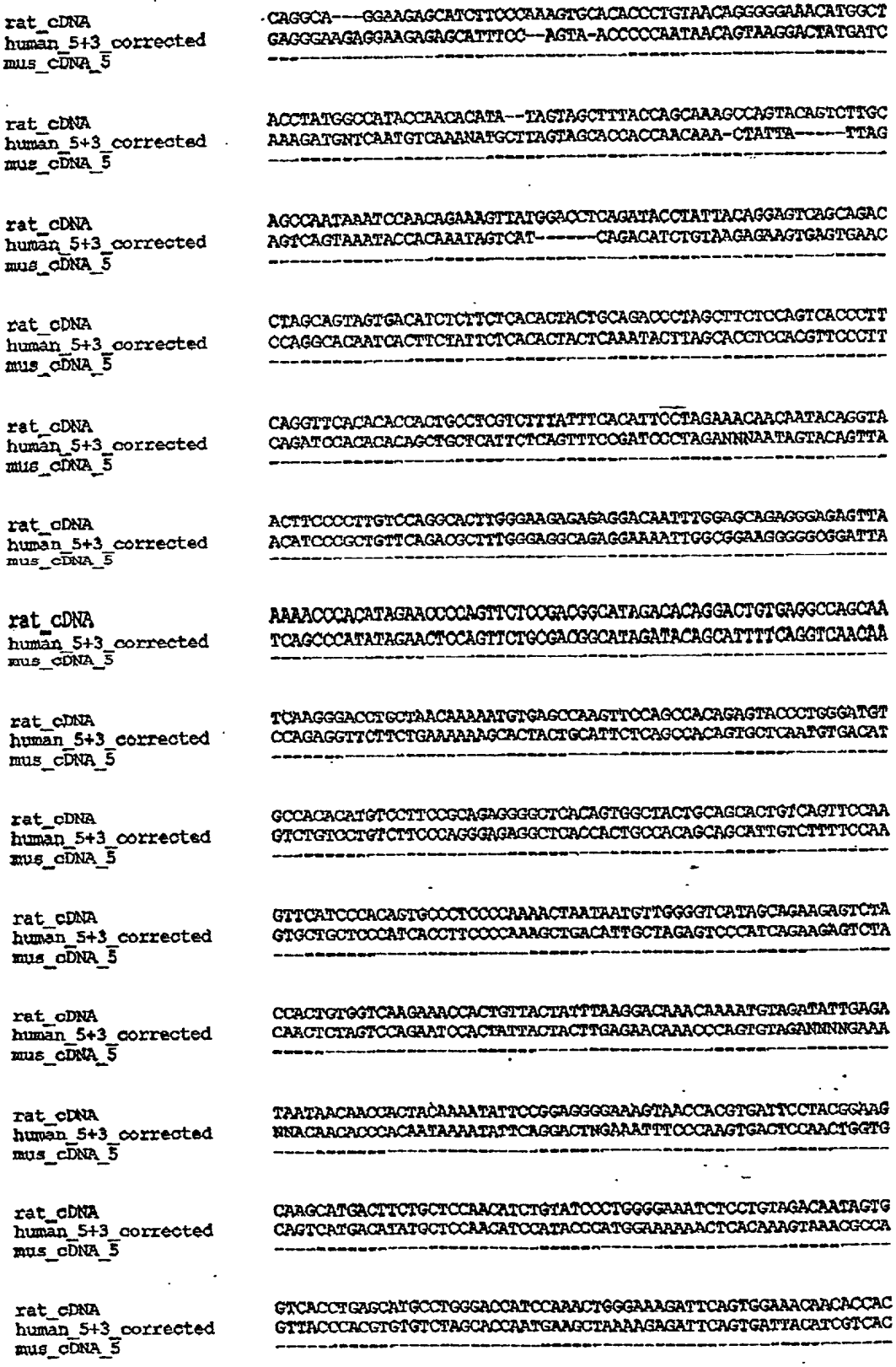
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human_5+3_corrected
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mus_cDNA_5               ------------------------------------------------------------

rat_cDNA                 GGAAAACTCCCTTGCACCAGATCTTTGTAAATAACCAGAAGAAGGAGGGGATGTTAAAGA
human_5+3_corrected      GGAAAATTCCCTGGCAACAGAACTTTGTAAATAACCATAACCCAAAAGGCAGATTAAGGA
mus_cDNA_5               ------------------------------------------------------------

rat_cDNA                 ATCCATATCAATTCGGTTTACAAAAGAACCCAGCCGCAAAGCTTCCCAAAATAGCTCCTC
human_5+3_corrected      ATCAACATAAAGTTAGTTTACAAAAAAGCACAGCTGTGATGCTTCCTAAAACATCTCCTG
mus_cDNA_5               ------------------------------------------------------------

rat_cDNA                 TTTTACCCACAG-GTCAGAGTTCCCCCTCAGATTCTACAACTCTCTTGACAAGTCCGCCA
human_5+3_corrected      CTTTACC-ACAGAGACAAAGTTCCCCTTTCCATTTCACCACACTTTCAACAAGTGTGATG
mus_cDNA_5               ------------------------------------------------------------

rat_cDNA                 CCAGCTCTGTCTACAACAATGGCTGCCACTCAGAACAAGGGCACTGAAGTAGTATCAGGT
human_5+3_corrected      CAAATTCCATCTAATACCTTGACTACCGCTCACCACACTACGACCAAA--ACACACAA-T
mus_cDNA_5               ------------------------------------------------------------

rat_cDNA                 GCCAGAAGTCTCTCAGCAGGGAAGAAGCAGCCCTTCACCAACTCCTCTCCAG-TGCTTCC
human_5+3_corrected      CCTGGAAGTCTTCCAACAAAGAAGGAGCTTCCCTTC-CCACCCCTTAACCCTATGCTTCC
mus_cDNA_5               ------------------------------------------------------------

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human_5+3_corrected      TAGTATTATAAGCAAAGACTCAAGTACAAAAAGCATCATATCAACGCAAACAGCAACCGC
mus_cDNA_5               ------------------------------------------------------------

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rat_cDNA                 CTCAACAACCTCTCTTCTGGCCA---TAACTGAACTGTTTGAG-AAGTAC--ACCCAGAC
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mus_cDNA_5               ------------------------------------------------------------

rat_cDNA                 AGTGAAAAGAGCCTCA---GACAC---ACCACCACCACTCCTCAGCAGTGGGGCGCCCCC
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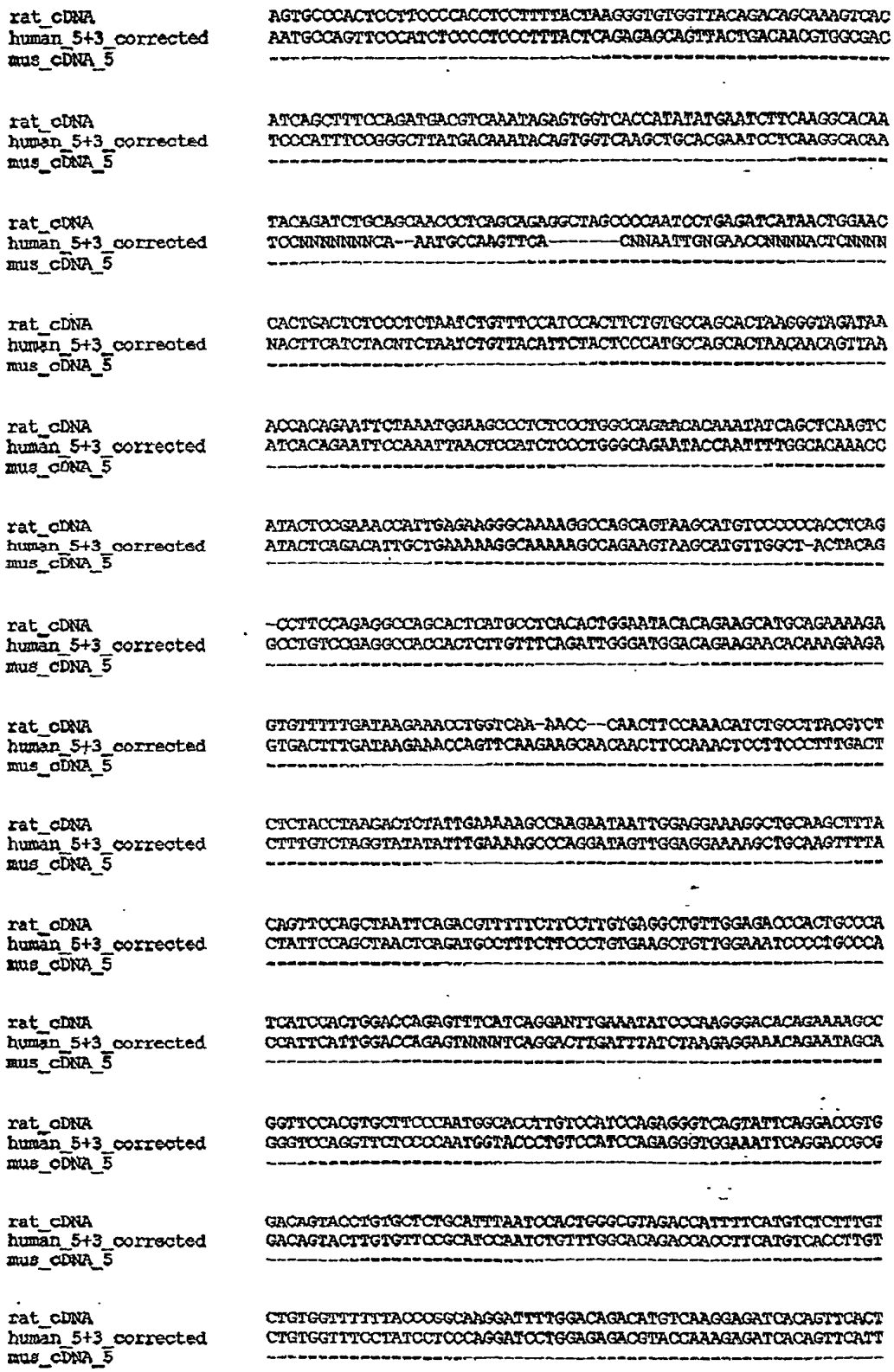
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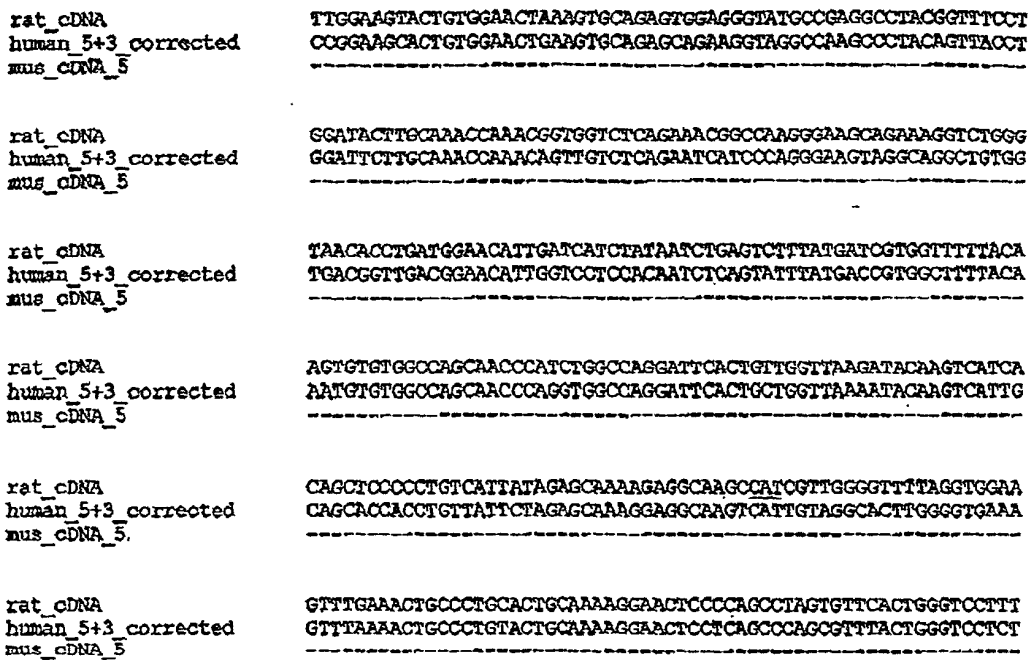
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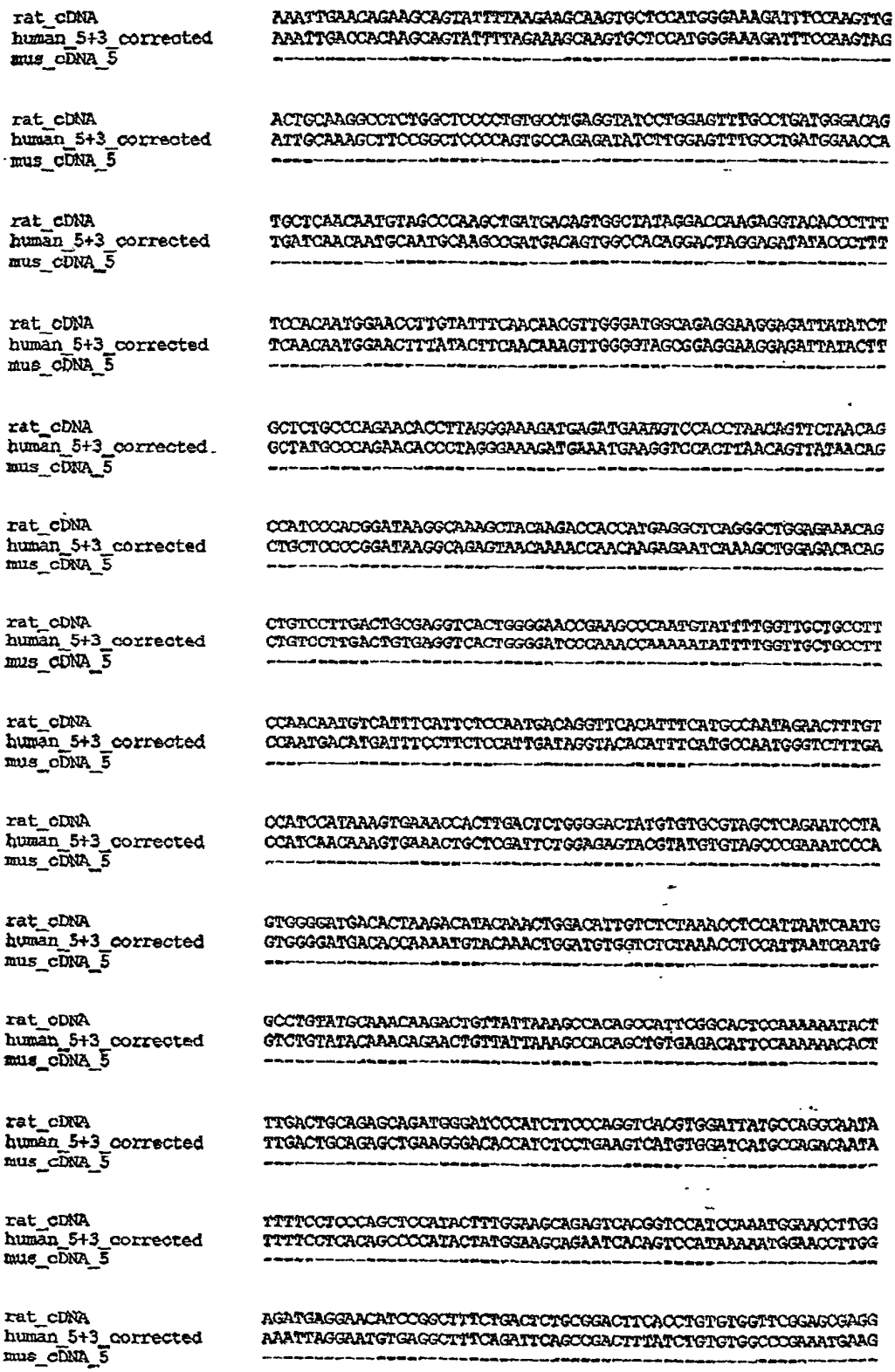
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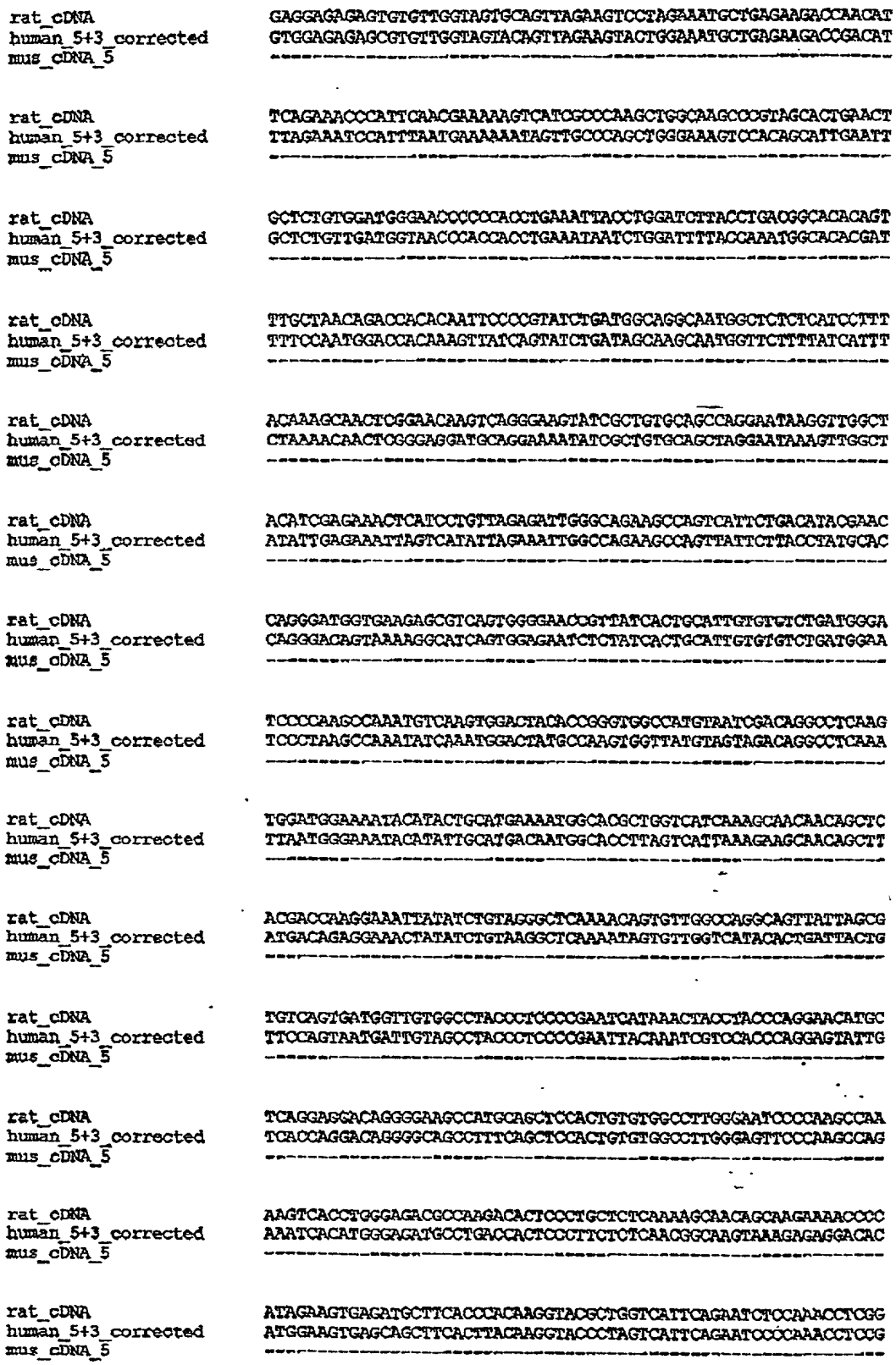
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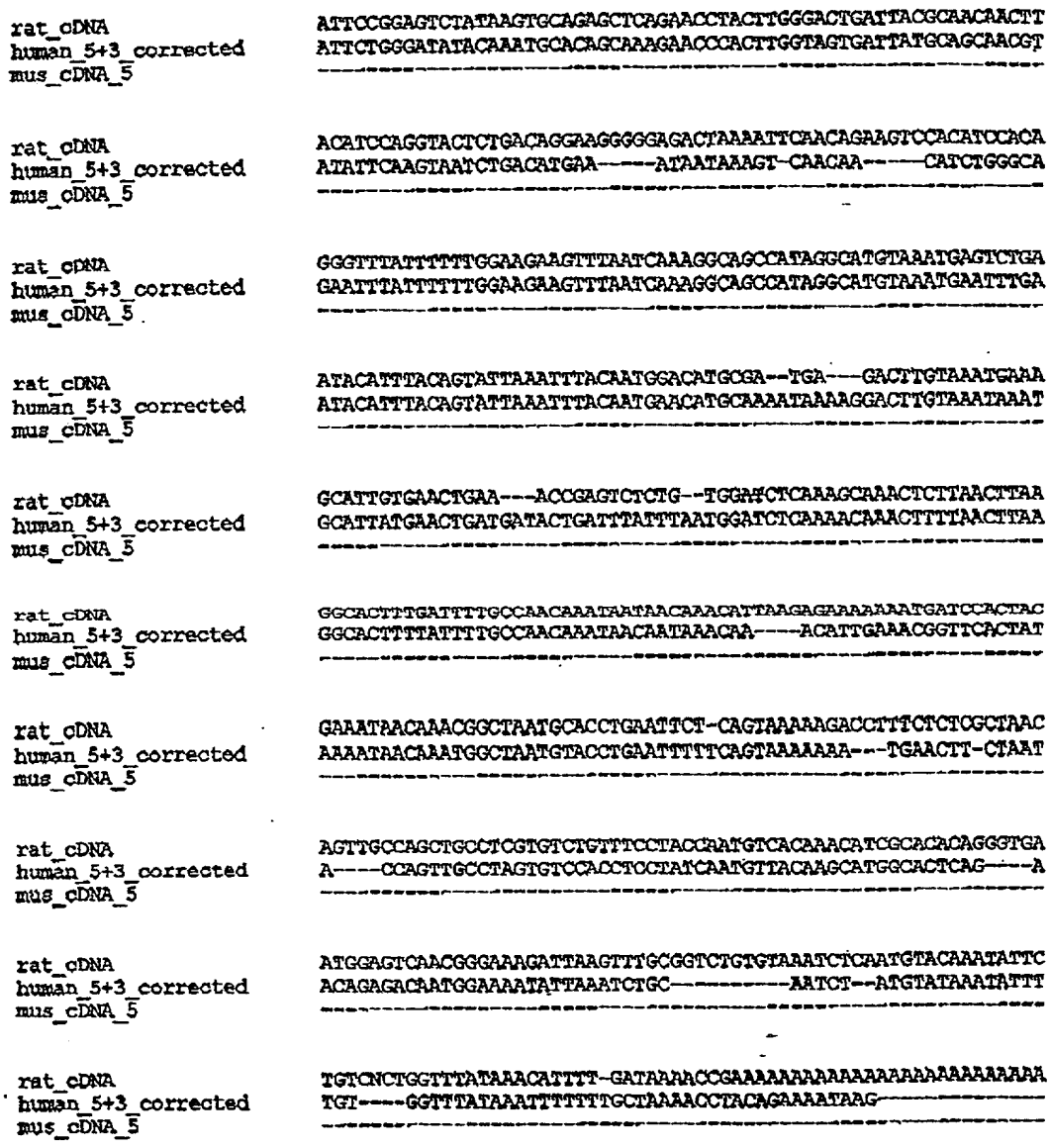

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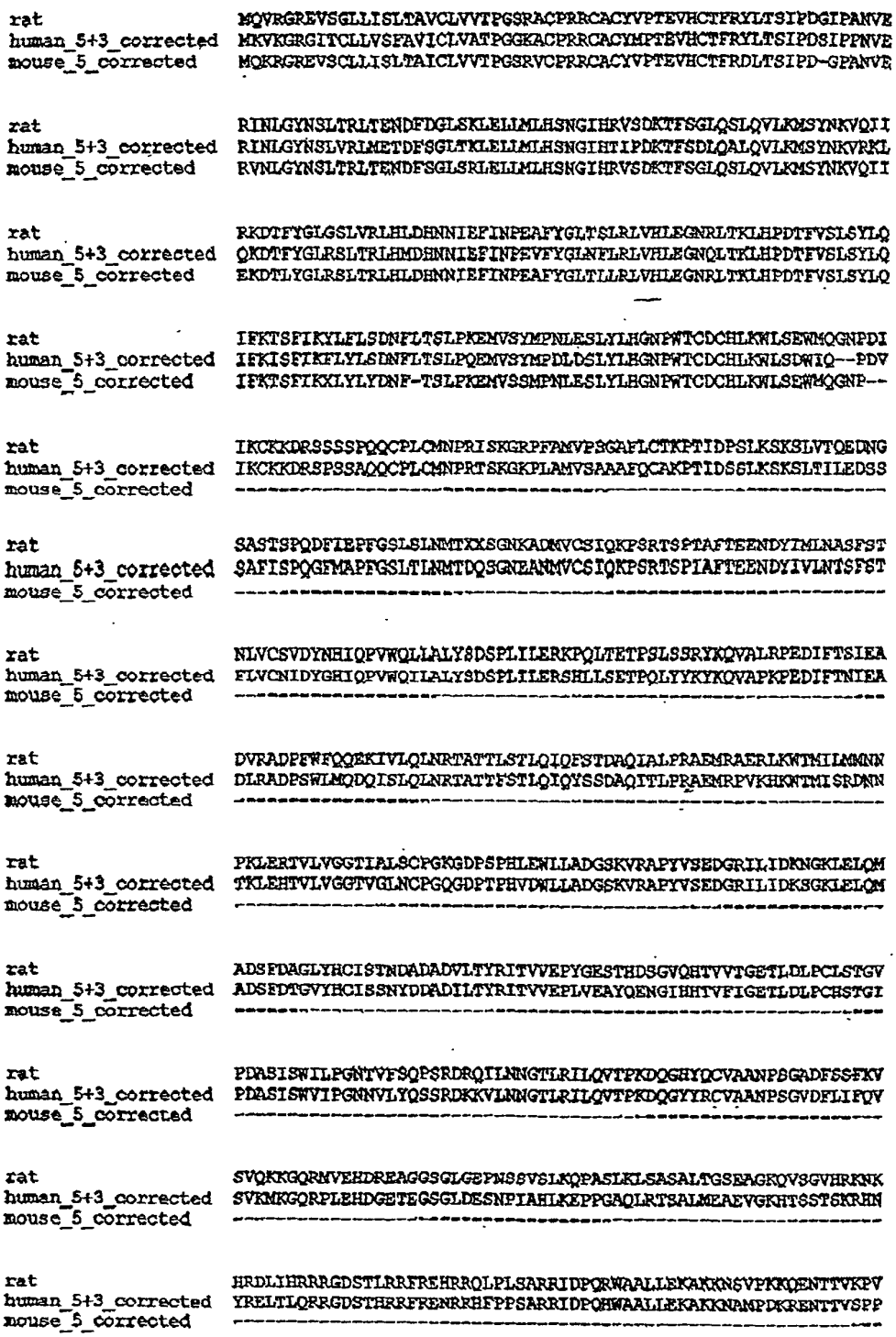
Figure 15



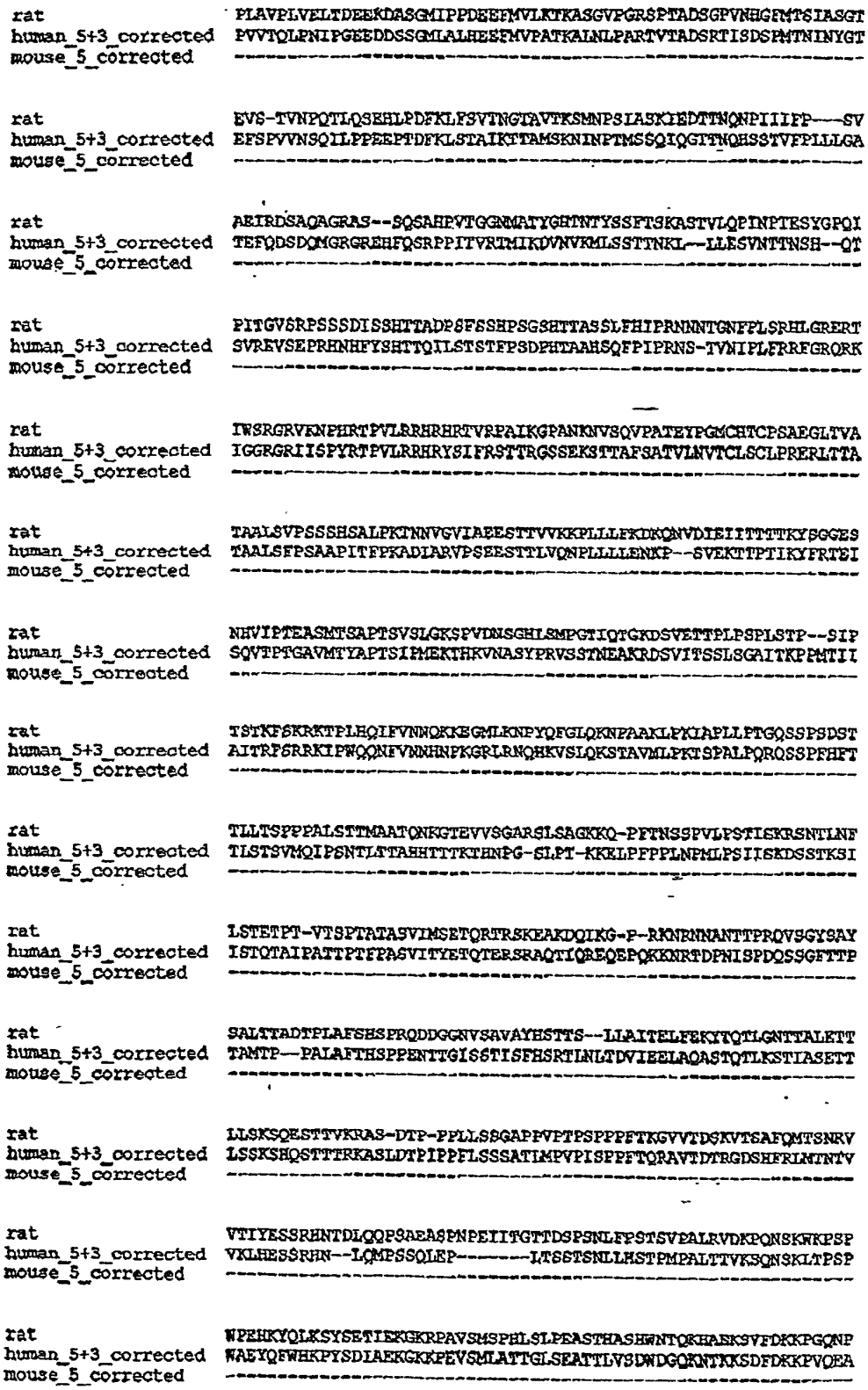

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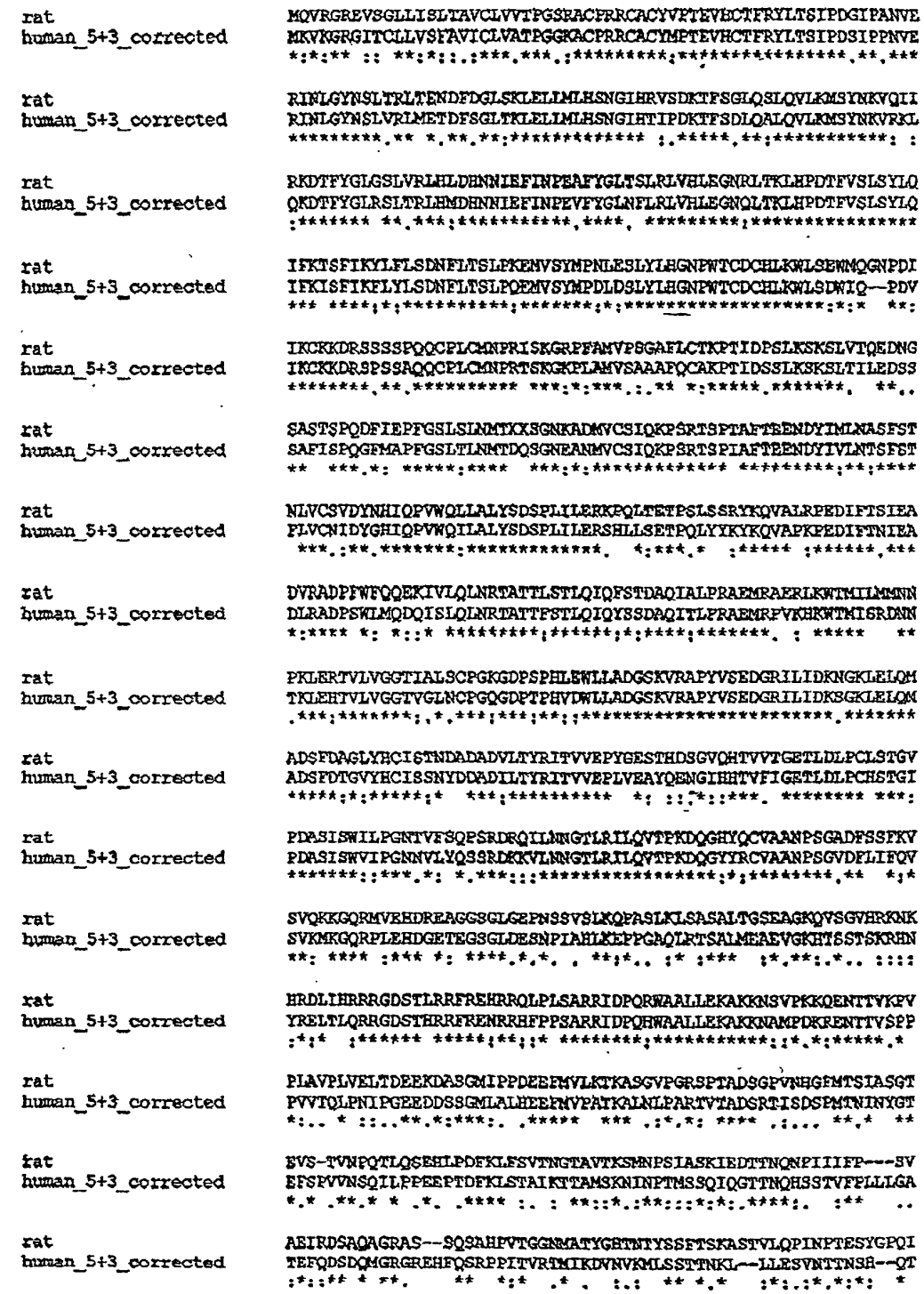
Figure 16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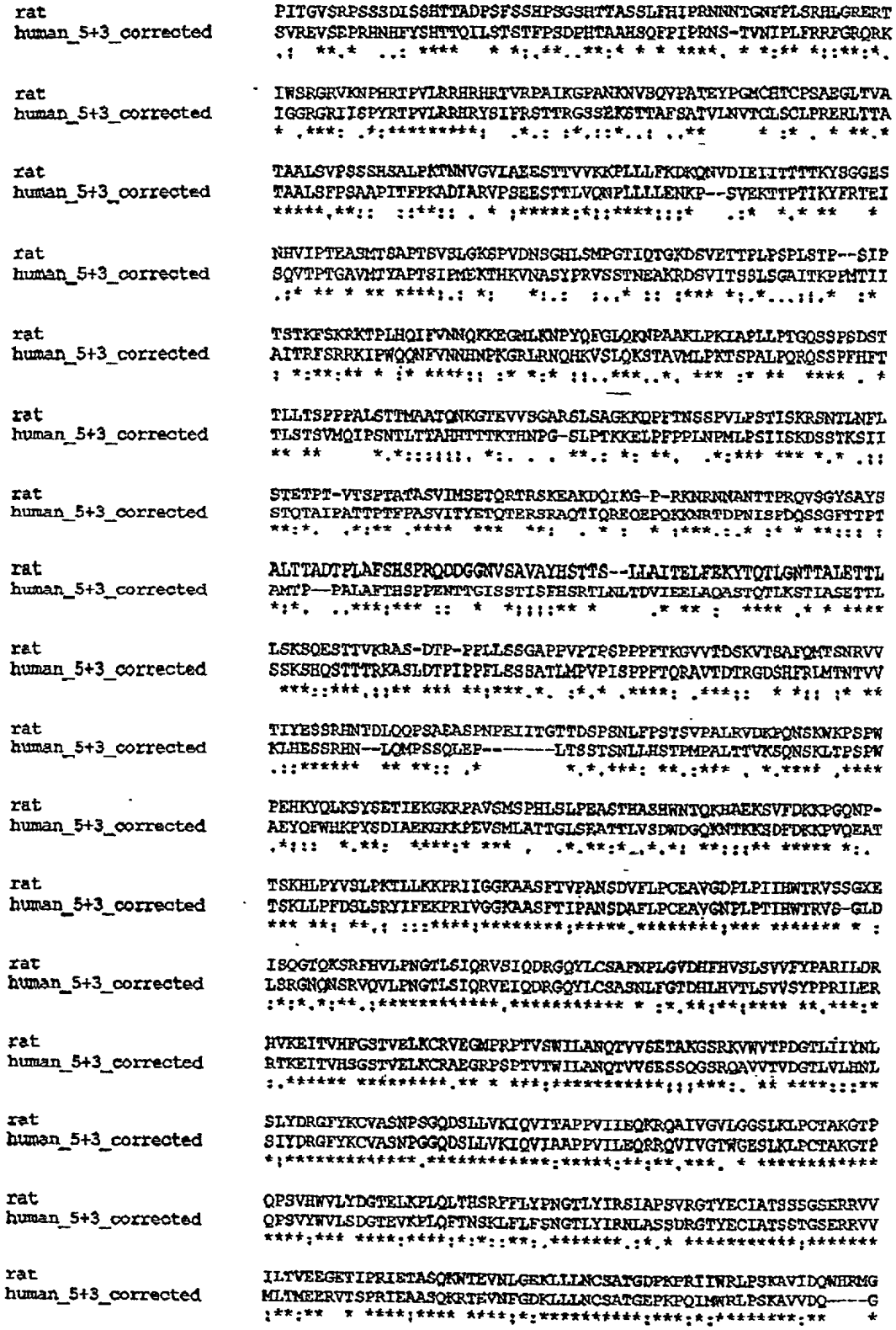
human_5+3_corrected
EVS-TVNPQTLQSEHLPDFKLFSVTNGTAVTKSMNPSIASKIEDTTNQNPIIIFP---SV
EFSPVVNSQILPPEEPTDFKLSTAIKTTAMSKNINPTMSSQIQGTTNQHSSTVFPLLLGA
rat
human_5+3_corrected
AEIRDSAQAGRAS--SQSAHPVTGGNMATYGHTNTYSSFTSKASTVLQPINPTESYGPQI
TEFQDSDQMGRGREHFQSRPPITVRTMIKDVNVKMLSSTTNKL--LLESVNTTNSH--QT


rat
human_5+3_corrected
PITGVSRPSSSDISSHTTADPSFSSHPSGSHTTASSLFHIPRNNNTGNFPLSRHLGRERT
SVREVSEPRHNHFYSHTTQILSTSTFPSDPHTAAHSQFPIPRNS-TVNIPLFRRFGRQRK
rat
human_5+3_corrected
IWSRGRVKNPHRTPVLRRHRHRTVRPAIKGPANKNVSQVPATEYPGMCHTCPSAEGLTVA
IGGRGRIISPYRTPVLRRHRYSIFRSTTRGSSEKSTTAFSATVLNVTCLSCLPRERLTTA
rat
human_5+3_corrected
TAALSVPSSSHSALPKTNNVGVIAEESTTVVKKPLLLFKDKQNVDIEIITTTTKYSGGES
TAALSFPSAAPITFPKADIARVPSEESTTLVQNPLLLLENKP--SVEKTTPTIKYFRTEI
rat
human_5+3_corrected
NHVIPTEASMTSAPTSVSLGKSPVDNSGHLSMPGTIQTGKDSVETTPLPSPLSTP--SIP
SQVTPTGAVMTYAPTSIPMEKTHKVNASYPRVSSTNEAKRDSVITSSLSGAITKPPMTII
rat
human_5+3_corrected
TSTKFSKRKTPLHQIFVNNQKKEGMLKNPYQFGLQKNPAAKLPKIAPLLPTGQSSPSDST
AITRFSRRKIPWQQNFVNNHNPKGRLRNQHKVSLQKSTAVMLPATSPALPQRQSSPFHFT
rat
human_5+3_corrected
TLLTSPPPALSTPMAATQNKGTEVVSGARSLSAGKKQPFTNSSPVLPSTISKRSNTLNFL
TLSTSVMQIPSNTLTTAHTTTKTHNPG-SLPTKKELPFPPLNPMLPSIISKDSSTKSII
rat
human_5+3_corrected
STETPT-VTSPTATASVIMSETQRTRSKEAKDQIKG-P-RKNRNNANTTPRQVSGYSAYS
STQTAIPATTPTFPASVITYETQTERSRAQTIQREQEPQKKNRTDPNISPDQSSGFTTPT
rat
human_5+3_corrected
ALTTADTPLAFSHSPRQDDGGNVSAVAYHSTTS--LLAITELFEKYTQTLGNTTALETTL
AMTP---PALAFTHSPPENTTGISSTISFHSRTLNLTDVIEELAQASTQTLKSTIASETTL
rat
human_5+3_corrected
LSKSQESTTVKRAS-DTP-PPLLSSGAPPVPTRSPPPFTKGVVTDSKVTSAFQMTSNRVV
SSKSHQSTTTRKASLDTPIPPFLSSSATLMPVPISPPFTQRAVTDTRGDSHFRLMTNTVV
rat
human_5+3_corrected
TIYESSRHNTDLQQPSAEASPNPEIITGTTDSPSNLFPSTSVPALKVDKPQNSKWKPSPW
KLHESSRHN--LQMPSSQLEP--------LTSSTSNLLHSTPMPALTTVKSQNSKLTPSPW
rat
human_5+3_corrected
PEHKYQLKSYSETIEKGKRPAVSMSPHLSLPEASTHASHWNTQKHAEKSVFDKKPGQNP-
AEYQFWHKPYSDIAEKGKKPEVSMLATTGLSEATTLVSDWDGQKNTKKSDFDKKPVQEAT
rat
human_5+3_corrected
TSKHLPYVSLPKTLLKKPRIIGGKAASFTVPANSDVFLPCEAVGDPLPIIHWTRVSSGKE
TSKLLPFDSLSRYIFEKPRIVGGKAASFTIPANSDAFLPCEAVGNPLPTIHWTRVS-GLD
rat
human_5+3_corrected
ISQGTQKSRFHVLPNGTLSIQRVSIQDRGQYLCSAFNPLGVDHFHVSLSVVFYPARILDR
LSRGNQNSRVQVLPNGTLSIQRVEIQDRGQYLCSASNLFGTDHLHVTLSVVSYPPRILER
rat
human_5+3_corrected
HVKEITVHPGSTVELKCRVEGMPRPTVSWILANQTVVSETAKGSRKVWVTPDGTLIIYNL
RTKEITVHSGSTVELKCRAEGRPSPTVTWILANQTVVSESSQGSRQAVVTVDGTLVLHNL
rat
human_5+3_corrected
SLYDRGFYKCVASNPSGQDSLLVKIQVITAPPVIIEQKRQAIVGVLGGSLKLPCTAKGTP
SIYDRGFYKCVASNPGGQDSLLVKIQVIAAPPVILEQRRQVIVGTWGESLKLPCTAKGTP
rat
human_5+3_corrected
QPSVHWVLYDGTELKPLQLTHSRFFLYPNGTLYIRSIAPSVRGTYECIATSSSGSERRVV
QPSVYWVLSDGTEVKPLQFTNSKLFLFSNGTLYIRNLASSDRGTYECIATSSTGSERRVV
rat
human_5+3_corrected
ILTVEEGETIPRIETASQKNTEVNLGEKLLLNCSATGDPKPRIIWRLPSKAVIDQNHRMG
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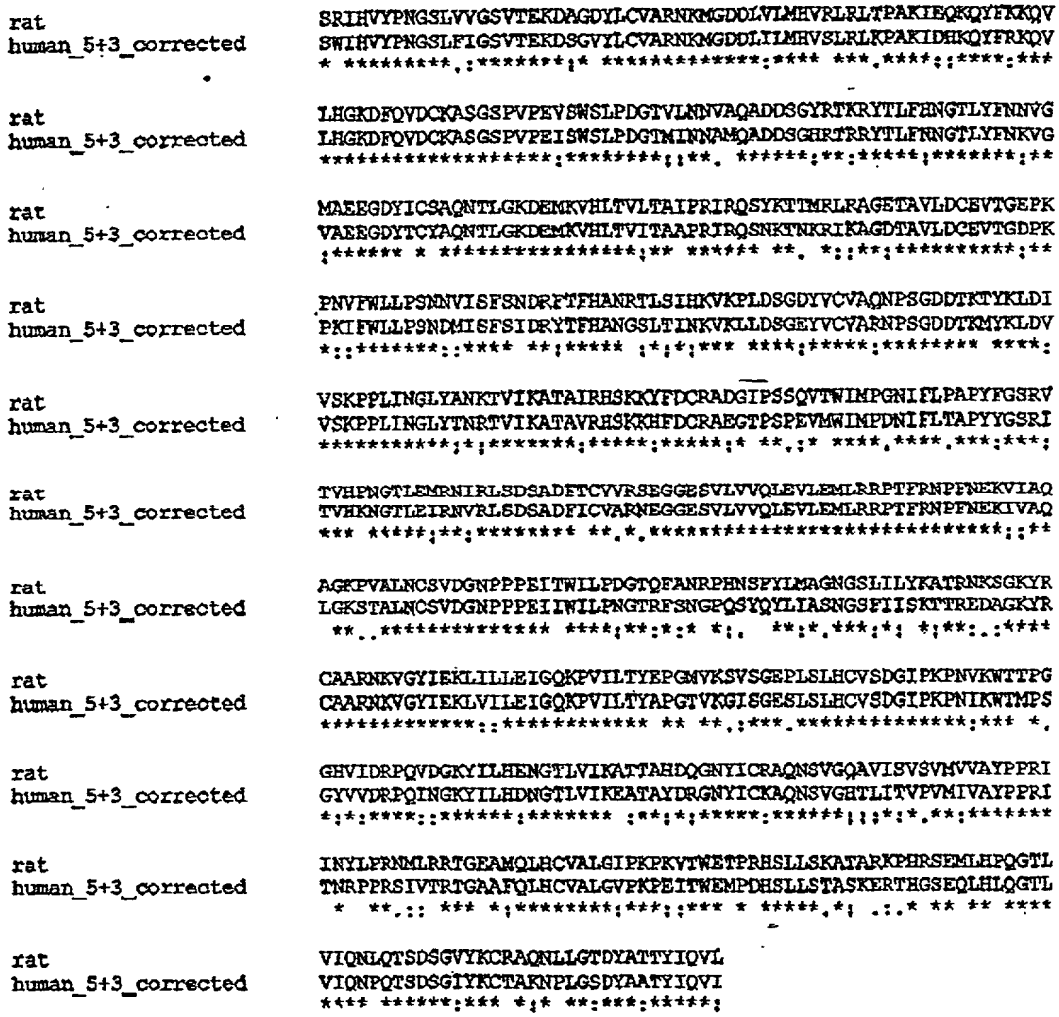

(rat: SEQ ID NO:13)
(human_5+3_corrected: SEQ ID NO:14)

Figure 17

MQKRGREVSCLLISLTAICLVVTPGSRVCPRRCACYVPTEVHCTFRDLTSIPDGPANVER
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KDTLYGLRSLTRLHLDHNNIEFINPEAFYGLTLLRLVHLEGNRLTKLHPDTFVSLSYLQIF
KTSFIKXLYLYDNFTSLPKEMVSSMPNLESLYLHGNPWTCDCHLKWLSEWMQGNP
(SEQ ID NO: 15)

Figure 18

MKVKGRGITCLLVSFAVICLVATPGGKACPRRCACYMPTEVHCTFRYLTSIPDSIPPNVE
RINLGYNSLVRLMETDFSGLTKLELLMLHSNGIHTIPDKTFSDLQALQVLKMSYNKVRK
LQKDTFYGLRSLTRLHMDHNNIEFINPEVFYGLNFLRLVHLEGNQLTKLHPDTFVSLSYL
QIFKISFIKFLYLSDNFLTSLPQEMSYMPDLDSLLYLHGNPWTCDCHLRWLSDWIQPDVI
KCKKDRSPSSAQQCPLCMNPRTSKGKPLAMVSAAAFQCAKPTIDSSLKSKSLTILEDSSS
AFISPQGFMAPFGSLTLNMTDQSGNEANMVCSIQKPSRTSPIAFTEENDYIVLNTSFSTFL
VCNIDYGHIQPVWQILALYSDSPLILERSHLLSETPQLYYKYKQVAPKPEDIFTNIEADLR
ADPSWLMQDQISLQLNRTATTFSTLQIQYSSDAQITLPRAEMRPVKHKWTMISRDNNTK
LEHTVLVGGTVGLNCPGQGDPTPHVDWLLADGSKVRAPYVSEDGRILIDKSGKLELQM
ADSFDTGVYHCISSNYDDADILTYRITVVEPLVEAYQENGIHHTVFIGETLDLPCHSTGIP
DASISWVIPGNNVLYQSSRDKKVLNNGTLRILQVTPKDQGYYRCVAANPSGVDFLIFQV
SVKMKGQRPLEHDGETEGSGLDESNPIAHLKEPPGAQLRTSALMEAEVGKHTSSTSKRH
NYRELTLQRRGDSTHRRFRENRRHFPPSARRIDPQHWAALLEKAKKNAMPDKRENTTV
SPPPVVTQLPNIPGEEDDSSGMLALHEEFMVPATKALNLPARTVTADSRTISDSPMTNIN
YGTEFSPVVNSQILPPEEPTDFKLSTAILTTAMSKNINPTMSSQIQGTTNQHSSTVFPLLLG
ATEFQDSDQMGRGREHFQSRPPITVRTMIKDVNVKMLSSTTNKLLLESVNSHQTSVREV
SEPRHNHFYSHTTQILSTSTFPSDPHTAAHSQFPIPRNSTVNIPLFRRFGRQRKIGGRGRIIS
PYRTPVLRRHRYSIFRSTTRGSSEKSTTAFSATVLNVTCLSCLPRELTTATAALSFPSAAPI
TFPKADIARVPSEESTTLVQNPLLLLENKPSVEKTTPTIKYFRTEISQVTPTGAVMTYAPT
SIPMEKTHKVNASYPRVSSTNEAKRDSVITSSLSGAITKPPMTIIAITRFSRRKIPWQQNFV
NNHNPKGRLRNQHKVSLQKSTAVMLPKTSPALPQRQSSPFHFRRLSTSVMQIPSNTLTT
AHHTTTKTHNPGSLPTKKELPFPPLNPMLPSIISKDSSTKSIISTQTAIPATTPTFPASVITYE
TQTERSRAQTIQREQEPQKKNRTDPNISPDQSSGFTTPTAMTPPALAFTHSPPENTTGISST
ISFHSRTLNLTDVIEELAQASTQTLKSTIASETTLSSKSHQSTTTRKASLDTPIPPFLSSSAT
LMPVPISPPFTQRAVTDTRGDSHFRLMTNTVVKLHESSRHNLQMPSSQLEPLTSSTSNLL
HSTPMPALTTVKSQNSKLTPSPWAEQFWHKPYSDIAEKGKKPEVSMLATTGLSEATTLV
SDWDGQKNTKKSDFDKKPVQEATTSKLLPFDSLSRYIFEKPRIVGGKAASFTIPANSDAF
LPCEAVGNPLPTIHWTRVSGLDLSRGNQNSRVQVLPNGTLSIQRVEIQDRFQYLCSASNL
FGTDHLHVTLSVVSYPPRILERRTKEITVHSGSTVELKCRAEGRPSPTVTWILANQTVVSE
SSQGSRQAVVTVDGTLVLHNLSIYDRGFYKCVASNPGGQDSLLVKIQVIAAPPVILEQRR
QVIVGTWGESLKLPCTAKGTPQPSVYWVLSDGTEVKPLQFTNSKLFLFSNGTLYIRNLAS

SDRFTYECIATSSTGSERRVVMLTMEERVTSPRIEAASQKRTEVNFGDKLLLNCSATGEP
KPQIMRLPSKAVVDQGSWIHYPNGSLFIGVTEKDSGVYLCVARNKMGDDLILMHVSLR
LKPAKIDHKQYFRKQVLHGKDFQVDCKASGSPVPEISWSLPDGTMINNAMQADDSGHR
TRRYRLFNNGTLYFNKVGVAEEGDYTCYAQNTLGKDEMKVHLTVITAAPRIRQSNKTN
KRIKAGDTAAVLDCEVTGDPKPKIFWLLPSNDMISFSIDRYTFHANGSLTINKVKLLDSG
EYVCVARNPSGDDTKMYKLDVVSKPPLINGLYTNRTVIKATAVRHSKKHFDCRAEGTP
SPEVMWIMPDNIFLTAPYYGSRITVHKNGTLEIRNVRLSADFICVARNEGGESVLVVQLE
VLEMLRRPTFRNPRNPFNEKIVAQLGKSTALNCVSVDGNPPPEIIWILPNGTRFSNGPQSY
QYLIASNGSFIISKTTREDAGKYRCAARNKVGYIEKLVILEIGQKPVILTYAPGTVKGISGE
SLSLHCVSDGIPKPNIKWTMPSGYVVDRPQINGKYILHDNGTLVIKEATAYDRGNYICKA
QNSVGHTLITVPVMIVAYPPRITNRPPRSIVTRTGAAFQLHCVALGVPKPEITWEMPDHS
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NO: 16)

Figure 19

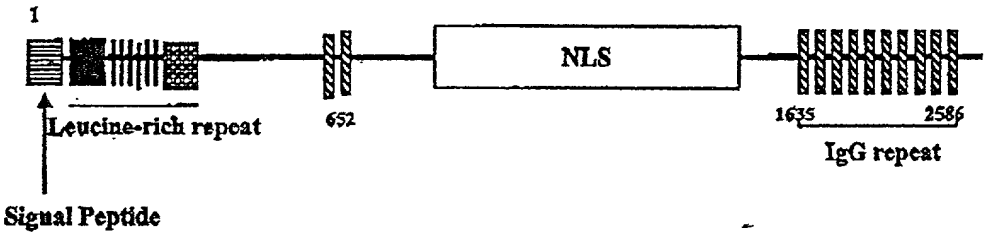
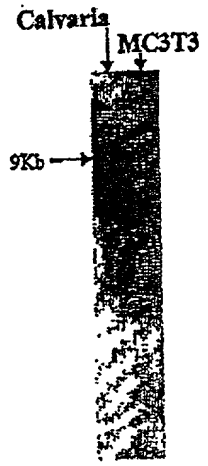


Figure 20

A



B

Cell lines & primary cells		
C6	Rat glioma	-
C2C12	Myoblasts	-
STO	Fibroblasts	-
Bone marrow	Stromal cells	- (+)
PC-3	prostatic carcinoma	-
SAOS-2	osteosarcoma	-
U2OS	osteosarcoma	+
Articular cartilage	chondrocytes	-
ROS	osteosarcoma	-
Calvaria	Osteoblasts	+
C3H10T1/2	mesenckyme	- (+)
MC3T3-E1	preosteoblastic	- (+)

Figure 21

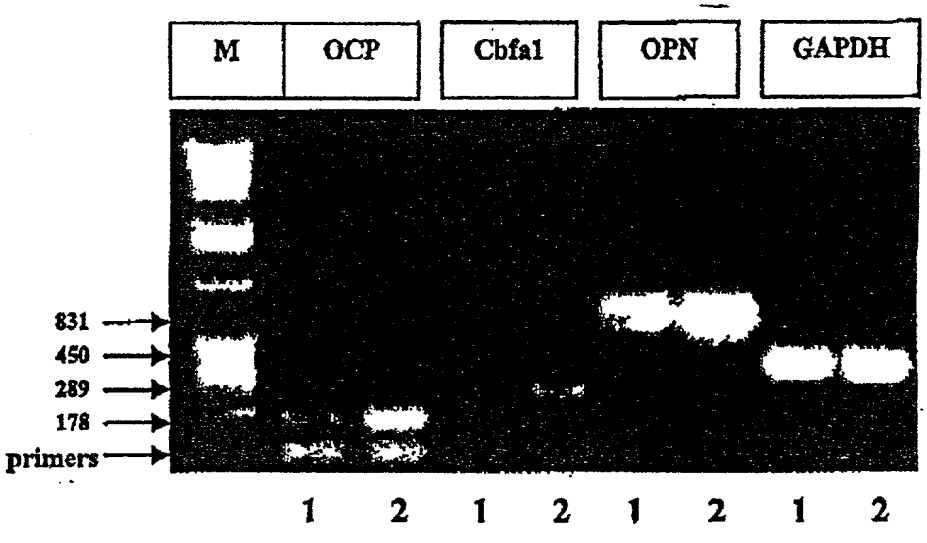


Figure 22

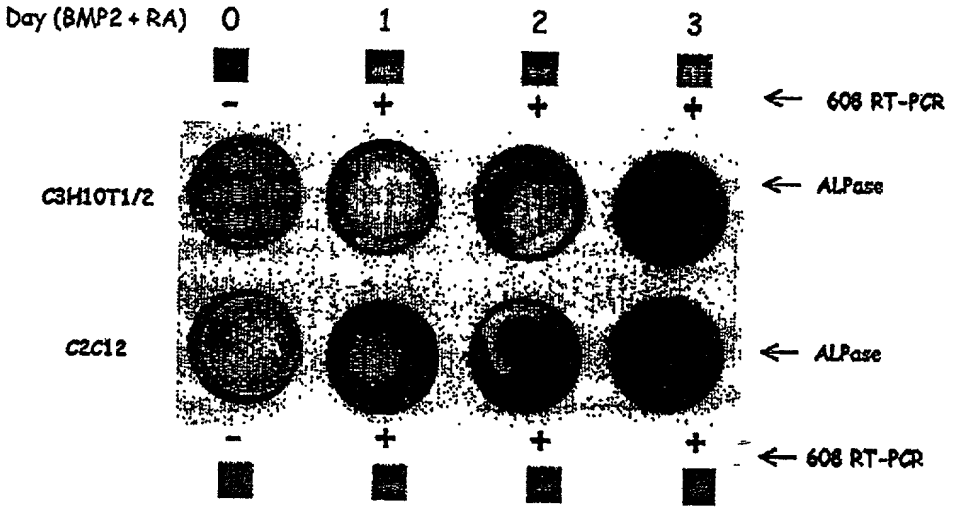


Figure 23

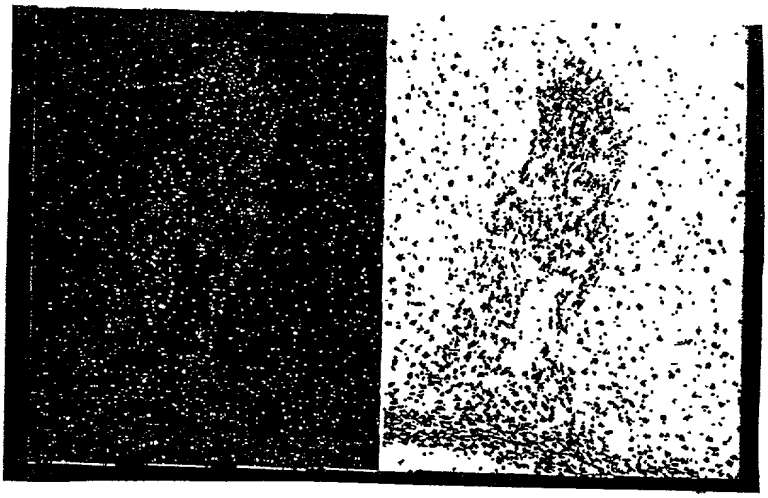


Figure 24

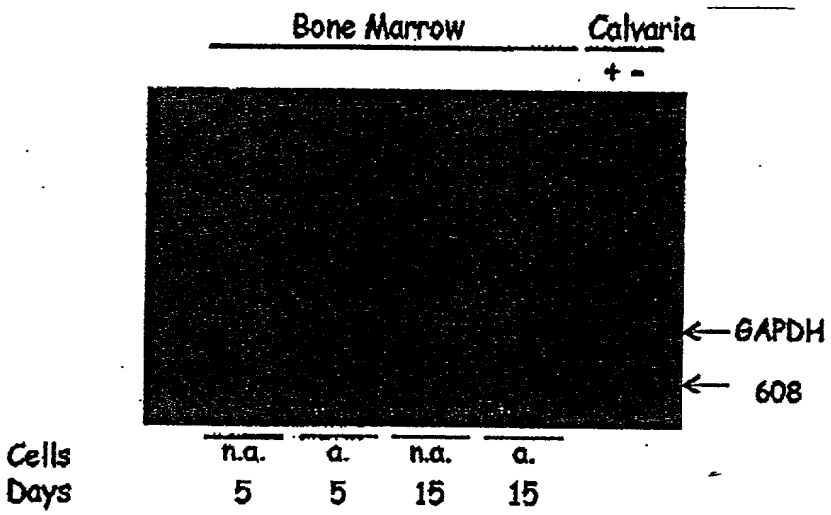


Figure 25

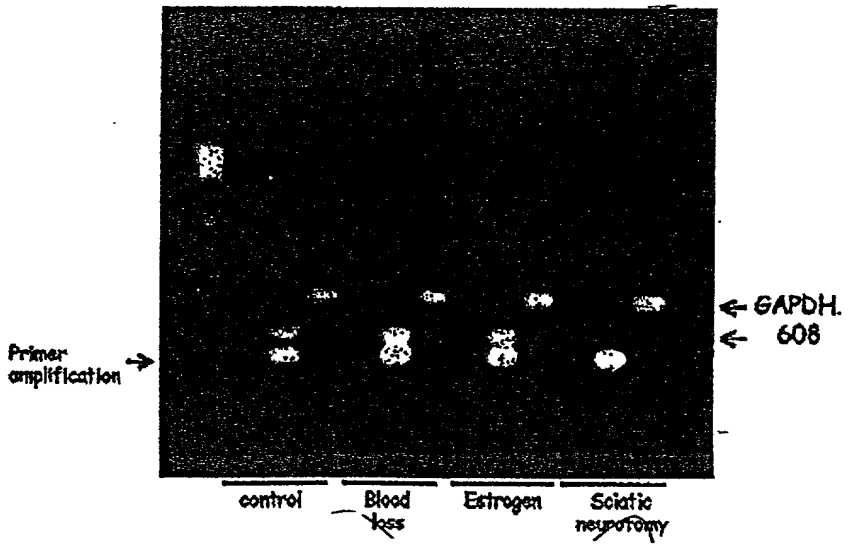


Figure 26

Figure 27

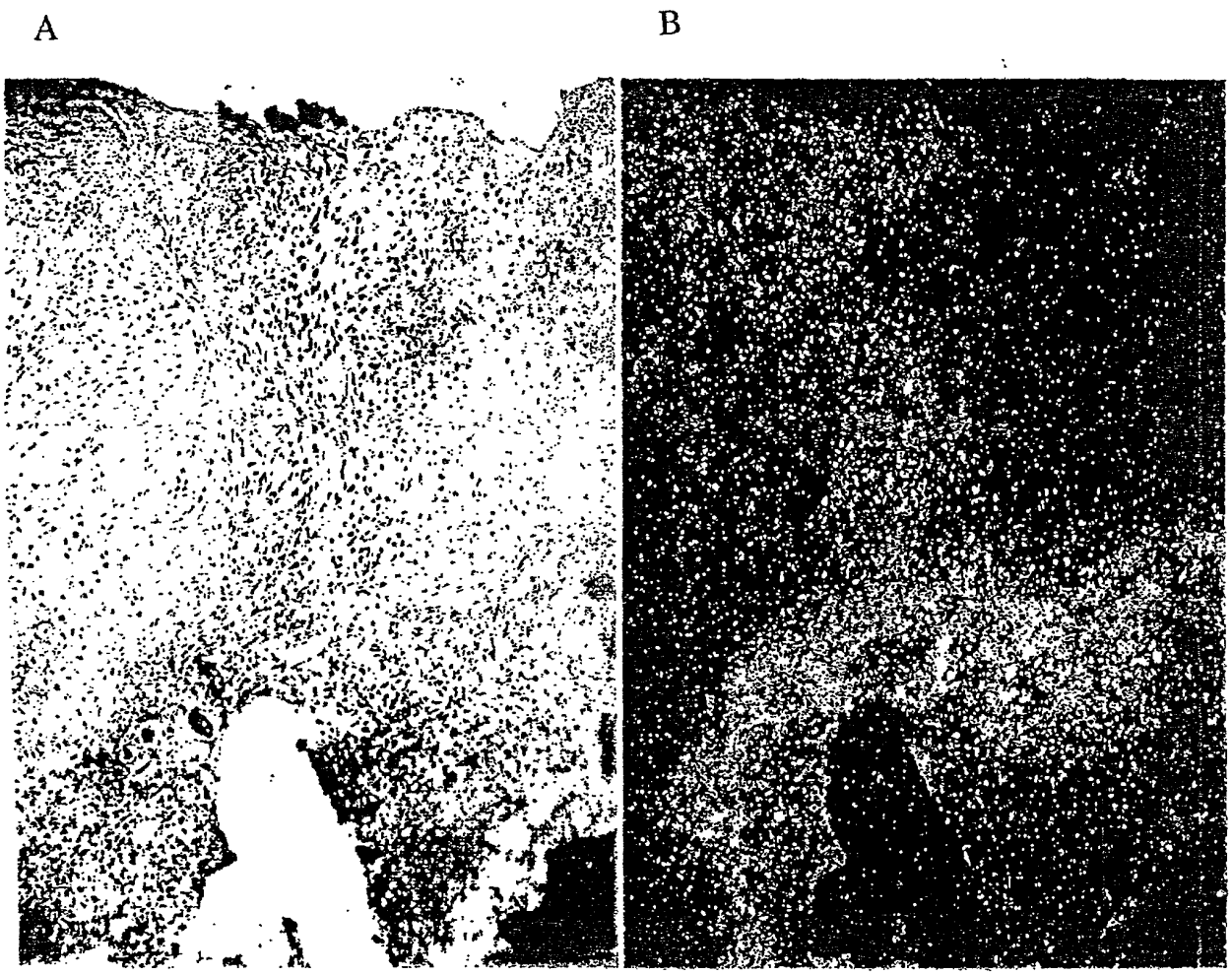


Figure 28

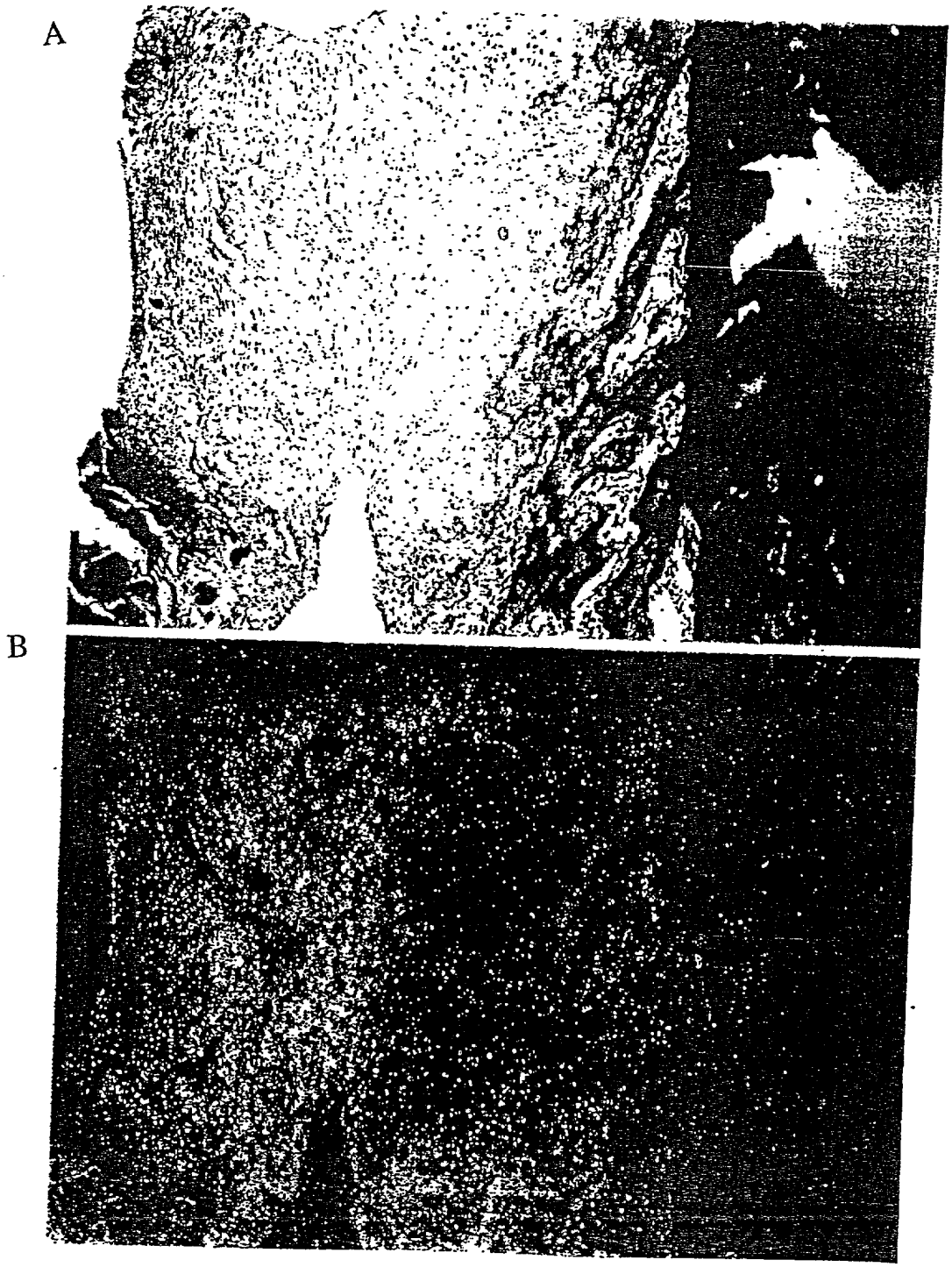


Figure 29

A

B

Figure 30

Figure 31

Figure 32

A

B

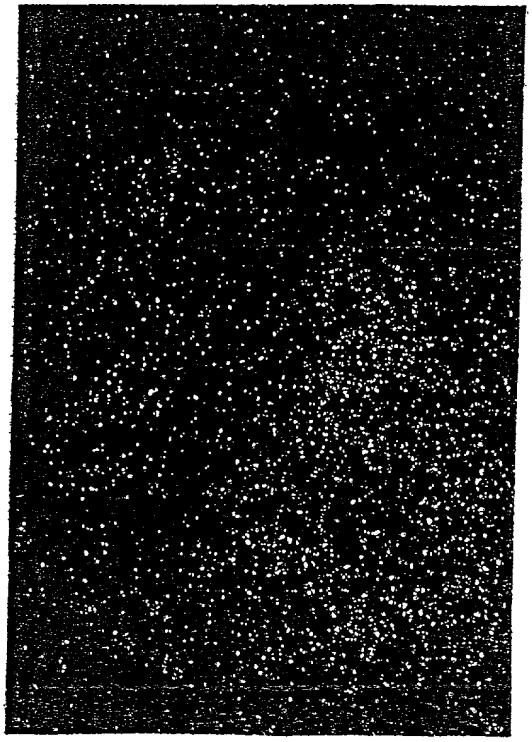


Figure 33

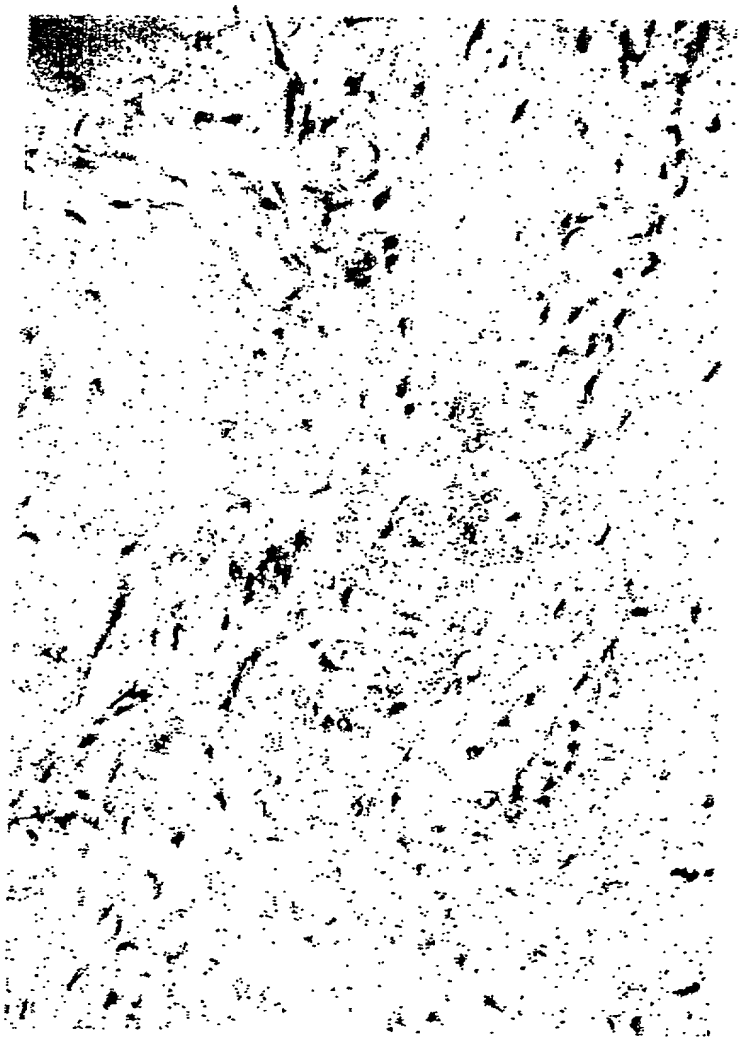


Figure 34

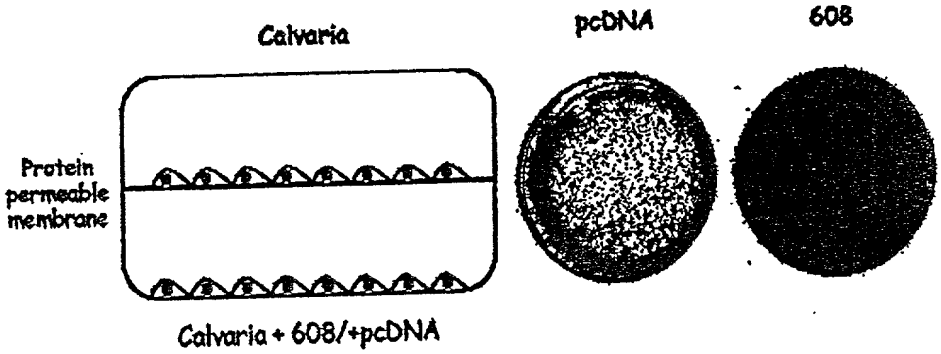


Figure 35

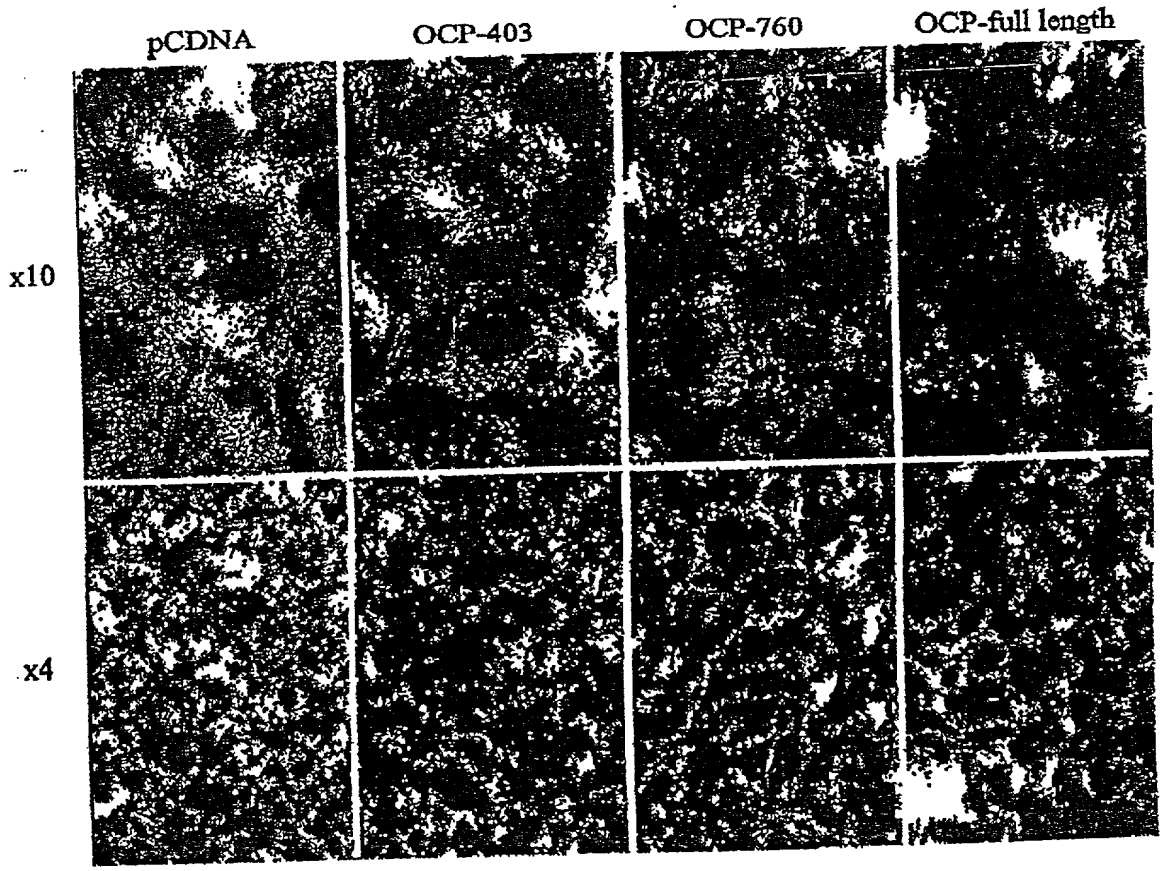


Figure 36

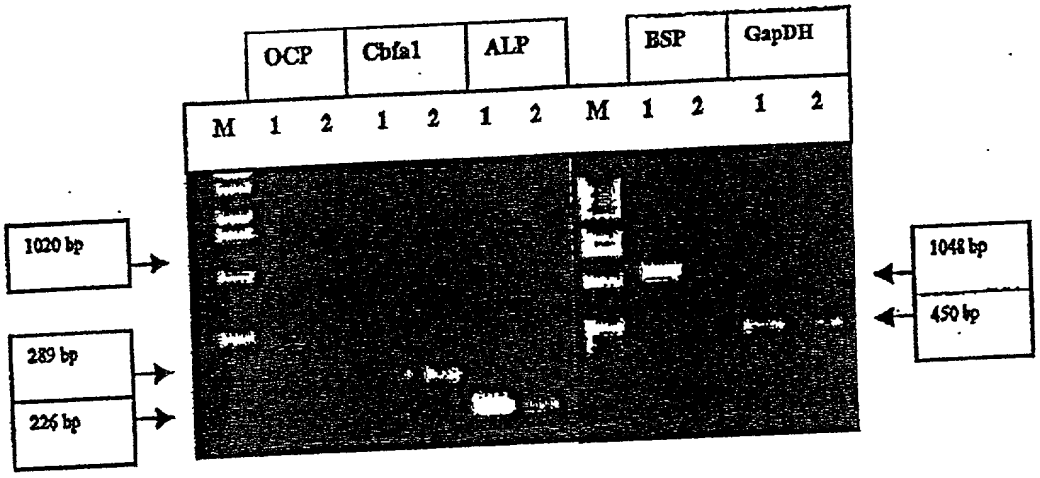


Figure 37

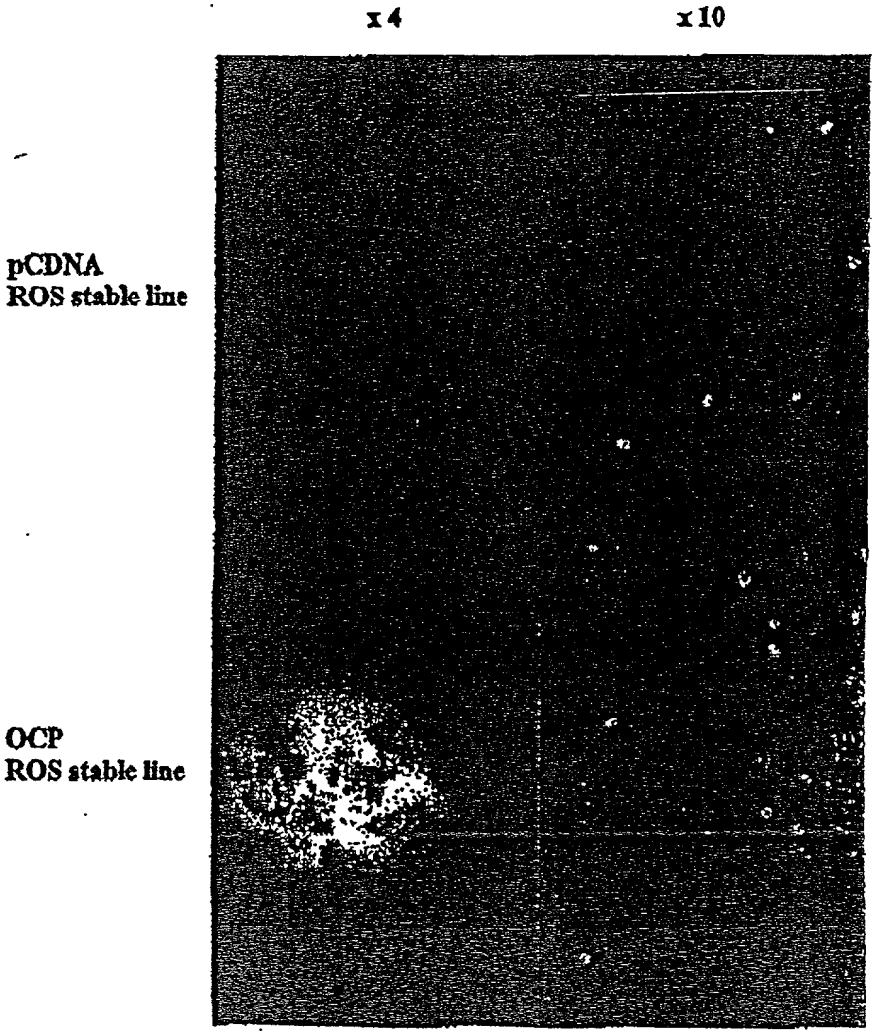


Figure 38

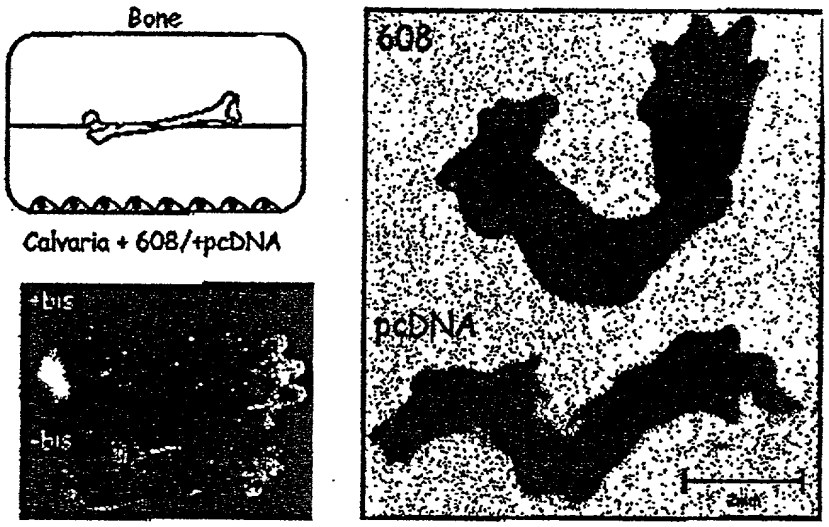


Figure 39

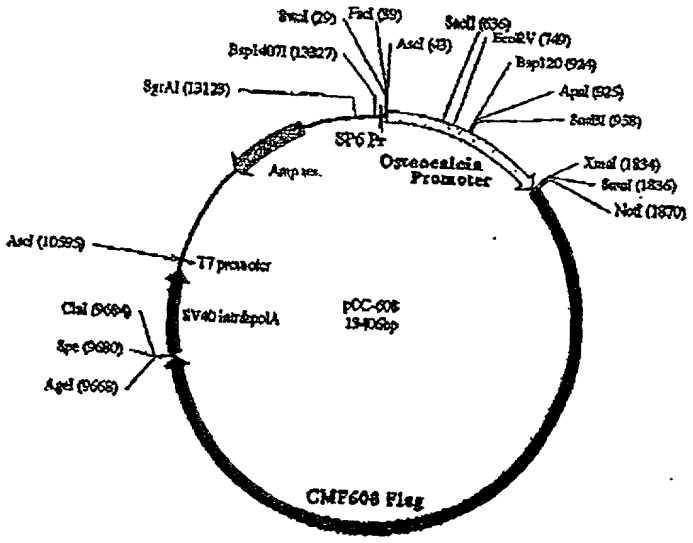


Figure 40

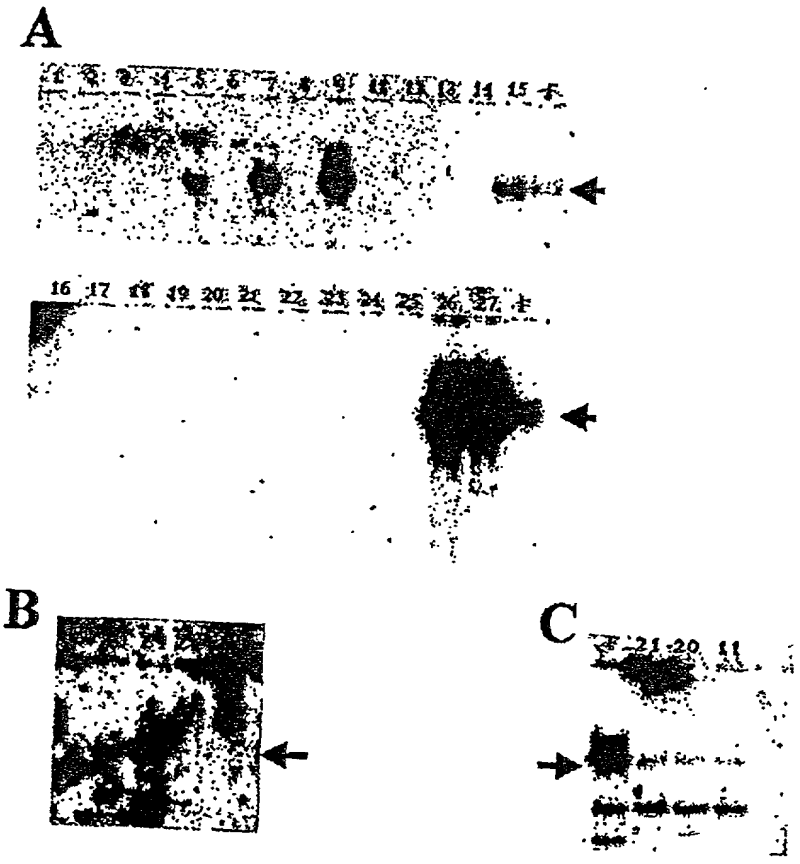


Figure 41

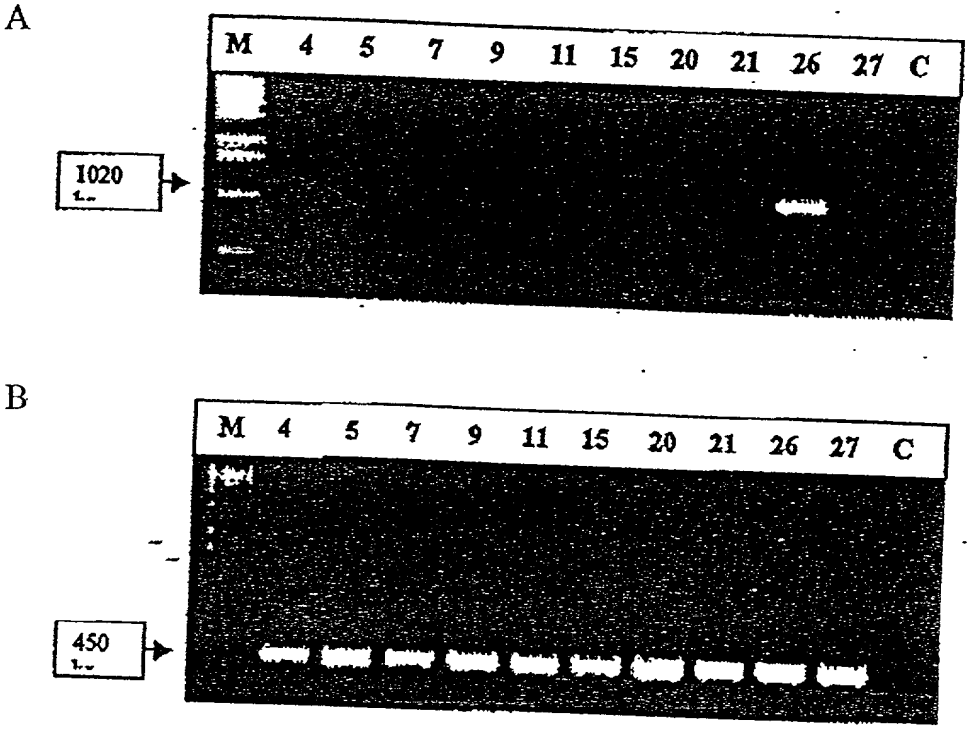
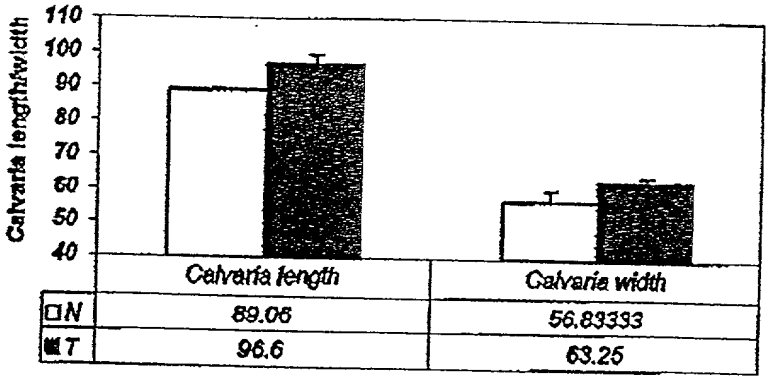


Figure 42



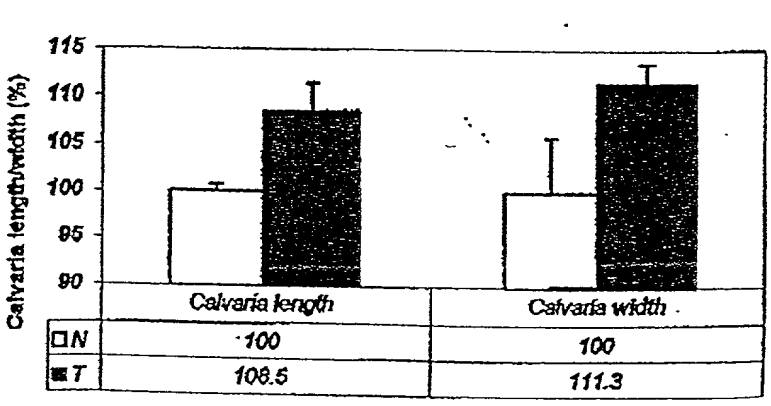


Figure 43

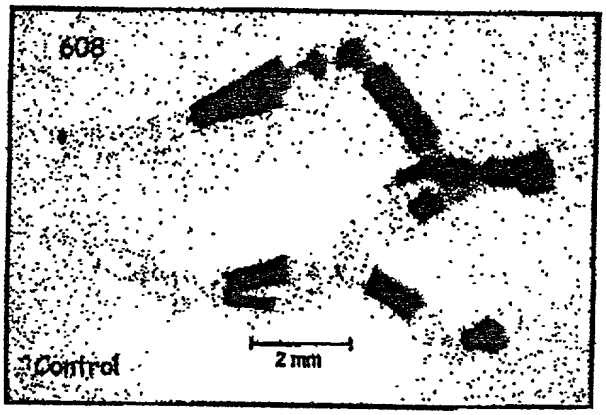


Figure 44

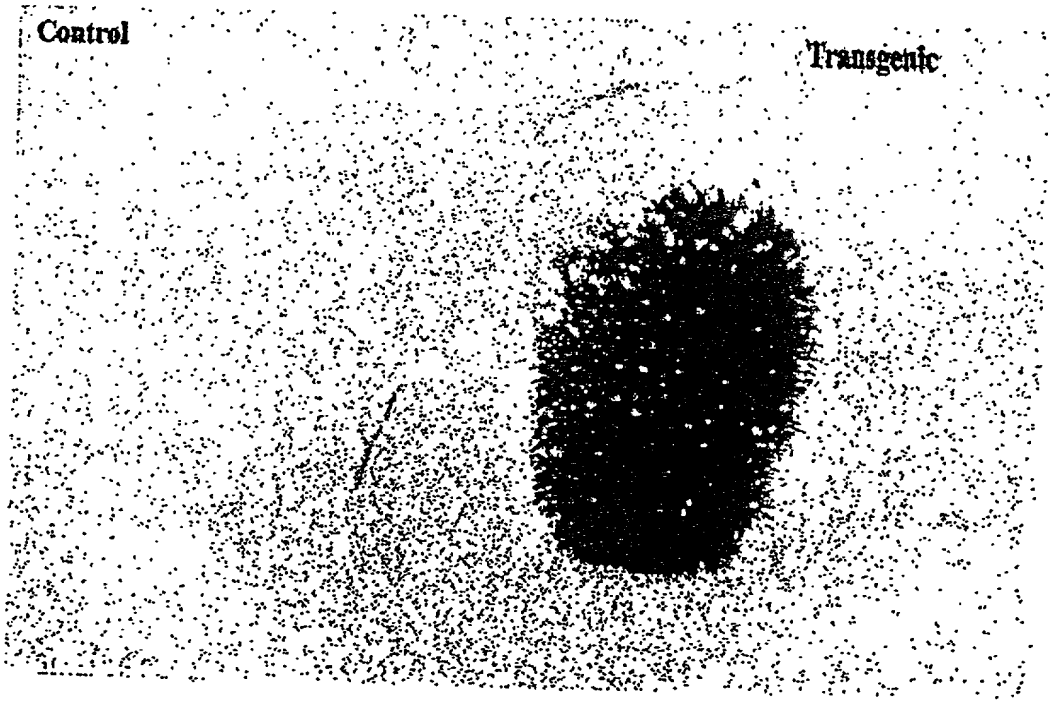


Figure 45

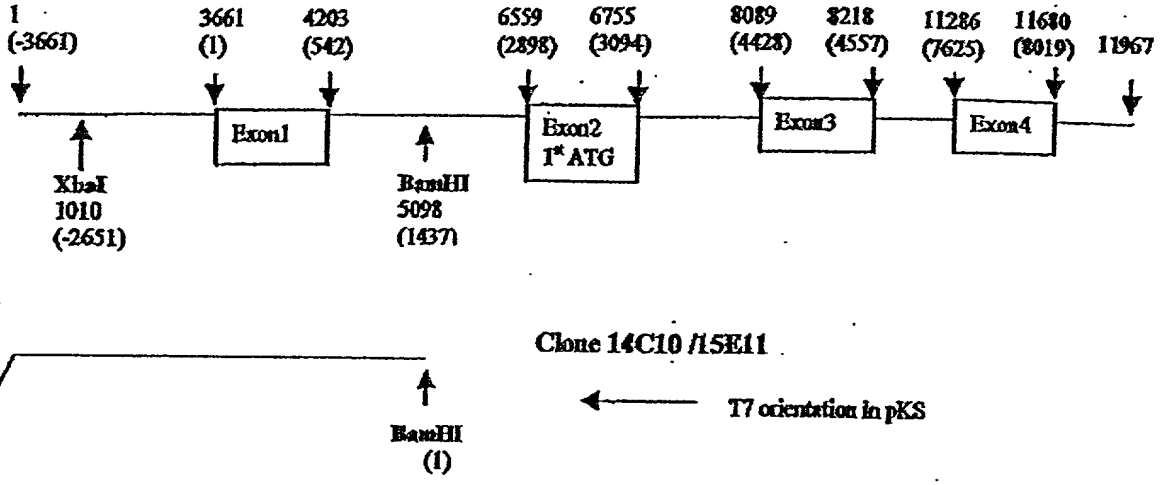


Figure 46

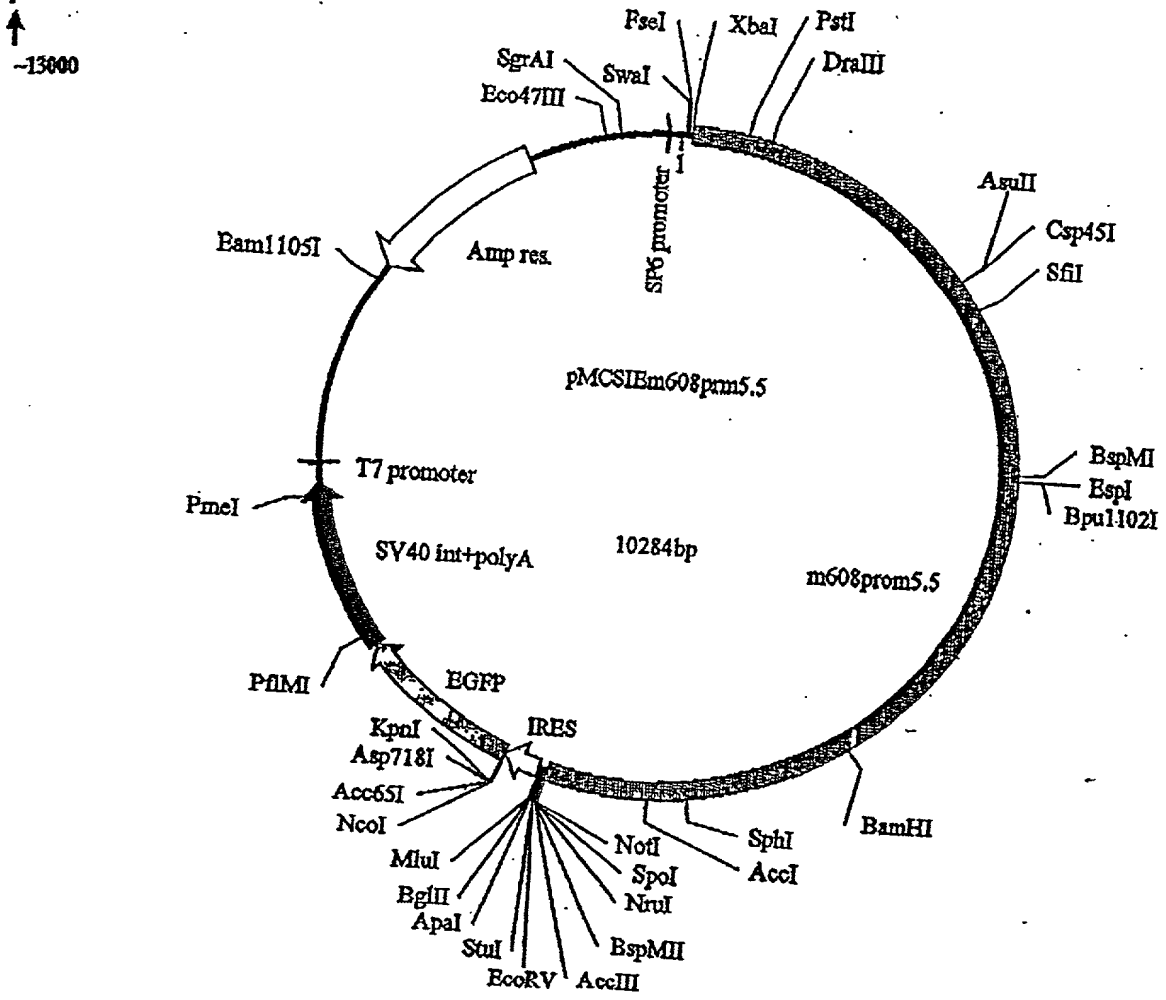


Figure 47

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CAGCTACCTTGTACCATCTTTGTTTATCTAATAATAGCAAGCTCATCTGCTTTTTAATCATC
ACGCAGAGAGTATTCAAAAATATTCAGTGATGTAACAGTGACAGTGTAGGCATAGAAGTA
ATCATTAGTAAATCTTAATTTGGGTTAAACTCATTCATAACAGCTCCAGGTTGGGAGGGAT
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CTTGGCCATGCTCCCCATCACTGTGTCAGTAAGCAGAGGGGTGTTTCCAAGCAGAGAAAG
AGCAGACAGTGTTATGCCTGCAAAGTCAGAGACTCAGCCCTCCCAGCTGGTCAGTTTACT
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(BamHI)
TTAATTGTCCCGATAACATTATTATGATCTCTAATGACAGGGATCCTGCTTTTCATTGGGA
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GGAAGCTAGCACACACTGGTTTATAAAGAGAACAGTTTCCTGAGTCTATGCAAGTTTACA
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CAGTTACGACTCTTAAAGAAAATATTCCCAATTATTCCCAGAGTTGCTATGTATGCTGTGC
CTAGGACTTTGCTTGAACTGGCCCTATAACTCTGGTGTGGTGTCTTTTCAGG – Artificial
NotI site

(SEQ ID NO:17)

Figure 48

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GAAACCTGCTGTGATCTCCATTTCTTCTCTGACCACATCCCCAAGTTATCACAAGGAGTTT
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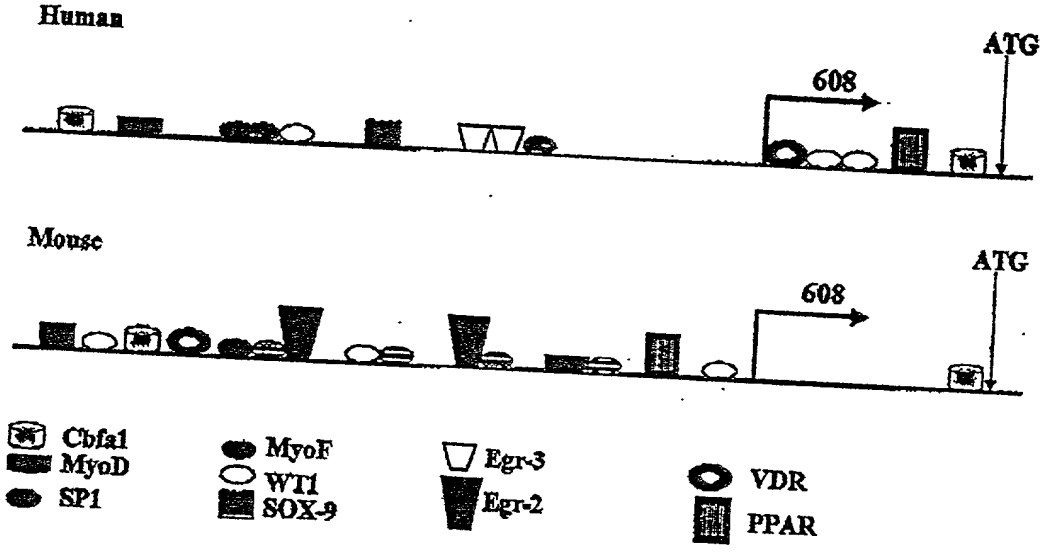
(SEQ ID NO:18)

Figure 49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Mouse
ATG
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Cbfa1
MyoD
SP1
MyoF
WT1
SOX-9
Egr-3
Egr-2
VDR
PPAR

Figure 50

TAAGCCTTTTGCTCCCGTTGGAAGCAAAGAACGTTCCTTCAATCAGGTGAAGGCTCT
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TGAGGCAATCTTGGAGAGGGAAAGGAAGCGGATGCGGGGCAGAGGCACACAGGAG
GACAGTGAGAGGGAAATGAACAAGAAAAAATGTGGACACATGCACAAAAATTCCA
TAGTCCACTACATTACTTTGTATTCTAATATTAAGAAAATAATAAACCCATTTCTGTG
CACTTATCACCCAGGCTCAACAGTTATCTTGGCCACAGATCCTGTCTCACTGCATCCT
GTCCACCTGAGTCCACTTAGCGTTCTGAATCCAATCCAGGGCATGATGCTTACTCCT
ACACAGAACTAAAGATTAAAGAGAGTTTAAAAGTAACCATGACATCTCTCTGTTCCT
TTAGCGATAAGTTCTTAATATTTATGGCTGCTTGTGTATGTTCTAATTTCTCTAATATT
GTCACATTTAGTTGGCAACTACTTTGTTTGAATTGAGTTGGAGTTAAGGTCCCATAG
GATTAATCTCAACATATTTCTATATTTATAAACTTTTCTCTCTTTGTGAAAGTTCCTTT
GAGAAAACAAATATGCCCATATCTTTCTTTACAGGTCTTAAAAATGAGCTATAACAA
AGTCCAAATAATTGAGAAGGATACTTTGTATGGACTCAGGAGCTTGACCCGGTTGCA
CCTGGATCACAACAACATTGAGTTTATCAACCCCGAGGCGTTTTACGGACTCACCTT
GCTCCGCTTGGTACATCTAGAAGGAAACCGGCTGACAAAGCTCCATCCAGACACAT
TTGTCTCTTTGAGCTATCTCCAGATATTTAAAACCTCCTTCATTAAGNACCTGTACTT
GTATGATAACTTCATTGACCTCCCTCCCAAAAGAAATGGTCTCCTCTATGCCAAACC
TAGAAAGCCTTTACTTGCATGGAAACCCATGGACCTGTGACTGCCATTTAAAGTGGT
TGTCCGAGTGGATGCAGGGAAACCCAGGTAACTATCTTGTTTGTTTGTTTCTTTTTTT
ATARKACGTATTTTCCTCAATTTCATTTAGAATGATATCCCAAAAGTCCCCCATAACC
TCCCCCCCACTTCCCTACCTACCCATTCCCATTTTTTGGCCCTGGCATTCCCCTGTACT
GGGGCATATAAAGTTTGCGTGTCCAATGGACCTCTCTTTCCAGTGATGGCCAACTAG
GCCATCTTTTGATACATATGCAGCTAGAGTCAAGAGCTCTGGGGTACTGGTTAGTTC
ATAATGTTGTTGCACCTACAGGGTTGAA (SEQ ID NO:20)

Figure 51

MPKRAHWGALSVVLILLWGHPRVALACPHPCACYVPSEVHCTFRSLASVPAGIARHVE
RINLGFNSIQALSETSFAGLTKLELLMIHGNEIPSIPDGALRDLSSLQVFKFSYNKLRVITG
QTLQGLSNLMRLHIDHNKIEFIHPQAFNGLTSLRLLHLEGNLLHQLHPSTFSTFTFLDYFR
LSTIRHLYLAENMVRTLPASMLRNMPLLENLYLQGNPWTCDCEMRWFLEWDAKSRGIL
KCKKDKAYEGGQLCAMCFSPKKLYKHEIHKLKDMTCLKPSIESPLRQNRSRSIEEEQEQ
EEDGGSQLILEKFQLPQWSISLNMTDEHGNMVNLVCDIKKPMDVYKIHLNQTDPPDIDIN
ATVALDFECPMTRENYEKLWKLIAYYSEVPVKLHRELMLSKDPRVSYQYRQDADEEAL
YYTGVRAQILAEPEWVMQPSIDIQLNRRQSTAKKVLLSYYTQYSQTISTKDTRQARGRS
WVMIEPSGAVQRDQTVLEGGPCQLSCNVKASESPSIFWVLPDGSILKAPMDDPDSKFSIL
SSGWLRIKSMEPSDSGLYQCIAQVRDEMDRMVYRVLVQSPSTQPAEKDTVTIGKNPGES
VTLPCNALAIPEAHLSWILPNRRIINDLANTSHVYMLPNGTLSIPKVQVSDSGYYRCVAV
NQQGADHFTVGITVTKKGSGLPSKRGRRPGAKALSRVREDIVEDEGGSGMGDEENTSR
RLLHPKDQEVFLKTKDDAINGDKKAKKGRRKLKLWKHSEKEPETNVAEGRRVFESRRR
INMANKQINPERWADILAKVRGKNLPKGTEVPPLIKTTSPPSLSLEVTPPFPAVSPPSASP
VQTVTSAEESSADVPLLGEEEHVLGTISSASMGLEHNHNGVILVEPEVTSTPLEEVVDDL
SEKTEEITSTEGDLKGTAAPTLISEPYEPSPTLHTLDTVYEKPTHEETATEGWSAADVGSS
PEPTSSEYEPPLDAVSLAESEPMQYFDPDLETKSQPDEDKMKEDTFAHLTPTPTIWVNDS
STSQLFEDSTIGEPGVPGQSHLQGLTDNIHLVKSSLSTQDTLLIKKGMKEMSQTLQGGNM
LEGDPTHSRSSESEGQESKSITLPDSTLGIMSSMSPVKKPAETTVGTLLDKDTTTVTTTPR
QKVAPSSTMSTHPSRRRPNGRRRLRPNKFRHRHKQTPPTTFAPSETFSTQPTQAPDIKISS
QVESSLVPTAWVDNTVNTPKQLEMEKNAEPTSKGTPRRKHGKRPNKHRYTPSTVSSRA
SGSKPSPSPENKHRNIVTPSSETILLPRTVSLKTEGPYDSLDYMTTTRKIYSSYPKVQETLP
VTYKPTSDGKEIKDDVATNVDKHKSDILVTGESITNAIPTSRSLVSTMGEFKEESSPVGFP
GTPTWNPSRTAQPGRLQTDIPVTTSGENLTDPPLLKELEDVDFTSEFLSSLTVSTPFHQEE
AGSSTTLSSIKVEVASSQAETTTLDQDHLETTVAILLSETRPQNHTPTAARMKEPASSSPS
TILMSLGQTTTTKPALPSPRISQASRDSKENVFLNYVGNPETEATPVNNEGTQHMSGPNE
LSTPSSDRDAFNLSTKLELEKQVFGSRSLPRGPDSQRQDGRVHASHQLTRVPAKPILPTA
TVRLPEMSTQSASRYFVTSQSPRHWTNKPEITTYPSGALPENKQFTTPRLSSTTIPLPLHM
SKPSIPSKFTDRRTDQFNGYSKVFGNNNIPEARNPVGKPPSPRIPHYSNGRLPFFTNKTLSF
PQLGVTRRPQIPTSPAPVMRERKVIPGSYNRIHSHSTFHLDFGPPAPPLLHTPQTTGSPSTN
LQNIPMVSSTQSSISFITSSVQSSGSFHQSSSKFFAGGPPASKFWSLGEKPQILTKSPQTVSV
TAETDTVFPCEATGKPKPFVTWTKVSTGALMTPNTRIQRFEVLKNGTLVIRKVQVQDRG
QYMCTASNLHGLDRMVVLLSVTVQQPQILASHYQDVTVYLGDTIAMECLAKGTPAPQI
SWIFPDRRVWQTVSPVESRITLHENRTLSIKEASFSDRGVYKCVASNAAGADSLAIRLHV
AALPPVIHQEKLENISLPPGLSIHIHCTAKAAPLPSVRWVLGDGTQIRPSQFLHGNLFVFP
NGTLYIRNLAPKDSGRYECVAANLVGSARRTVQLNVQRAAANARITGTSPRRTDVRYG
GTLKLDCSASGDPWPRILWRLPSKRMIDALFSFDSRIKVFANGTLVVKSVTDK

DAGDYLCVARNKVGDDYVVLKVDVVMKPAKIEHKEENDHKVFYGGDLKVDCVATGL
PNPEISWSLPDGSLVNSFMQSDDSGGRTKRYVVFNNGTLYFNEVGMREEGDYTCFAEN
QVGKDEMRVRVKVVTAPATIRNKTYLAVQVPYGDVVTVACEAKGEPMPKVTWLSPTN
KVIPTSSEKYQIYQDGTLLIQKAQRSDSGNYTCLVRNSAGEDRKTVWIHVNVQPPKING
NPNPITTVREIAAGGSRKLIDCKAEGIPTPRVLWAFPEGVVLPAPYYGNRITVHGNGSLDI
RSLRKSDSVQLVCMARNEGGEARLIVQLTVLEPMEKPIFHDPISEKITAMAGHTISLNCS
AAGTPTPSLVWVLPNGTDLQSGQQLQRFYHKADGMLHISGLSSVDAGAYRCVARNAA
GHTERLVSLKVGLKPEANKQYHNLVSIINGETLKLPCTPPGAGQGRFSWTLPNGMHLEG
PQTLGRVSLLDNGTLTVREASVFDRGTYVCRMETEYGPSVTSIPVIVIAYPPRITSEPTPVI
YTRPGNTVKLNCMAMGIPKADITWELPDKSHLKAGVQARLYGNRFLHPQGSLTIQHAT
QRDAGFYKCMAKNILGSDSKTTYIHVF (SEQ ID NO: 21)

Figure 52

ATGCCCAAGC GCGCGCACTG GGGGGCCCTC TCCGTGGTGC TGATCCTGCT
TTGGGGCCAT CCGCGAGTGG CGCTGGCCTG CCCGCATCCT TGTGCCTGCT
ACGTCCCCAG CGAGGTCCAC TGCACGTTCC GATCCCTGGC TTCCGTGCCC
GCTGGCATTG CTAGACACGT GGAAAGAATC AATTTGGGGT TTAATAGCAT
ACAGGCCCTG TCAGAAACCT CATTTGCAGG ACTGACCAAG TTGGAGCTAC
TTATGATTCA CGGCAATGAG ATCCCAAGCA TCCCCGATGG AGCTTTAAGA
GACCTCAGCT CTCTTCAGGT TTTCAAGTTC AGCTACAACA AGCTGAGAGT
GATCACAGGA CAGACCCTCC AGGGTCTCTC TAACTTAATG AGGCTGCACA
TTGACCACAA CAAGATCGAG TTTATCCACC CTCAAGCTTT CAACGGCTTA
ACGTCTCTGA GGCTACTCCA TTTGGAAGGA AATCTCCTCC ACCAGCTGCA
CCCCAGCACC TTCTCCACGT TCACATTTTT GGATTATTTC AGACTCTCCA
CCATAAGGCA CCTCTACTTA GCAGAGAACA TGGTTAGAAC TCTTCCTGCC
AGCATGCTTC GGAACATGCC GCTTCTGGAG AATCTTTACT TGCAGGGAAA
TCCGTGGACC TGCGATTGTG AGATGAGATG GTTTTTGGAA TGGGATGCAA
AATCCAGAGG AATTCTGAAG TGTAAAAAGG ACAAAGCTTA TGAAGGCGGT
CAGTTGTGTG CAATGTGCTT CAGTCCAAAG AAGTTGTACA AACATGAGAT
ACACAAGCTG AAGGACATGA CTTGTCTGAA GCCTTCAATA GAGTCCCCTC
TGAGACAGAA CAGGAGCAGG AGTATTGAGG AGGAGCAAGA ACAGGAAGAG
GATGGTGGCA GCCAGCTCAT CCTGGAGAAA TTCCAACTGC CCCAGTGGAG
CATCTCTTTG AATATGACCG ACGAGCACGG GAACATGGTG AACTTGGTCT
GTGACATCAA GAAACCAATG GATGTGTACA AGATTCACTT GAACCAAACG
GATCCTCCAG ATATTGACAT AAATGCAACA GTTGCCTTGG ACTTTGAGTG
TCCAATGACC CGAGAAAACT ATGAAAAGCT ATGGAAATTG ATAGCATACT
ACAGTGAAGT TCCCGTGAAG CTACACAGAG AGCTCATGCT CAGCAAAGAC
CCCAGAGTCA GCTACCAGTA CAGGCAGGAT GCTGATGAGG AAGCTCTTTA
CTACACAGGT GTGAGAGCCC AGATTCTTGC AGAACCAGAA TGGGTCATGC
AGCCATCCAT AGATATCCAG CTGAACCGAC GTCAGAGTAC GGCCAAGAAG
GTGCTACTTT CCTACTACAC CCAGTATTCT CAAACAATAT CCACCAAAGA
TACAAGGCAG GCTCGGGGCA GAAGCTGGGT AATGATTGAG CCTAGTGGAG
CTGTGCAAAG AGATCAGACT GTCCTGGAAG GGGGTCCATG CCAGTTGAGC
TGCAACGTGA AAGCTTCTGA GAGTCCATCT ATCTTCTGGG TGCTTCCAGA
TGGCTCCATC CTGAAAGCGC CCATGGATGA CCCAGACAGC AAGTTCTCCA
TTCTCAGCAG TGGCTGGCTG AGGATCAAGT CCATGGAGCC ATCTGACTCA
GGCTTGTACC AGTGCATTGC TCAAGTGAGG GATGAAATGG ACCGCATGGT
ATATAGGGTA CTTGTGCAGT CTCCCTCCAC TCAGCCAGCC GAGAAAGACA
CAGTGACAAT TGGCAAGAAC CCAGGGGAGT CGGTGACATT GCCTTGCAAT
GCTTTAGCAA TACCCGAAGC CCACCTTAGC TGGATTCTTC CAAACAGAAG
GATAATTAAT GATTTGGCTA ACACATCACA TGTATACATG TTGCCAAATG
GAACTCTTTC CATCCCAAAG GTCCAAGTCA GTGATAGTGG

TTACTACAGA TGTGTGGCTG TCAACCAGCA AGGGGCAGAC CATTTTACGG
TGGGAATCAC AGTGACCAAG AAAGGGTCTG GCTTGCCATC CAAAAGAGGC
AGACGCCCAG GTGCAAAGGC TCTTTCCAGA GTCAGAGAAG ACATCGTGGA
GGATGAAGGG GGCTCGGGCA TGGGAGATGA AGAGAACACT TCAAGGAGAC
TTCTGCATCC AAAGGACCAA GAGGTGTTCC TCAAAACAAA GGATGATGCC
ATCAATGGAG ACAAGAAAGC CAAGAAAGGG AGAAGAAAGC TGAAACTCTG
GAAGCATTCG GAAAAAGAAC CAGAGACCAA TGTTGCAGAA GGTCGCAGAG
TGTTTGAATC TAGACGAAGG ATAAACATGG CAAACAAACA GATTAATCCG
GAGCGCTGGG CTGATATTTT AGCCAAAGTC CGTGGGAAAA ATCTCCCTAA
GGGCACAGAA GTACCCCCGT TGATTAAAAC CACAAGTCCT CCATCCTTGA
GCCTAGAAGT CACACCACCT TTTCCTGCTG TTTCTCCCCC CTCAGCATCT
CCTGTGCAGA CAGTAACCAG TGCTGAAGAA TCCTCAGCAG ATGTACCTCT
ACTTGGTGAA GAAGAGCACG TTTTGGGTAC CATTTCCTCA GCCAGCATGG
GGCTAGAACA CAACCACAAT GGAGTTATTC TTGTTGAACC TGAAGTAACA
AGCACACCTC TGGAGGAAGT TGTTGATGAC CTTTCTGAGA AGACTGAGGA
GATAACTTCC ACTGAAGGAG ACCTGAAGGG GACAGCAGCC CCTACACTTA
TATCTGAGCC TTATGAACCA TCTCCTACTC TGCACACATT AGACACAGTC
TATGAAAAGC CCACCCATGA AGAGACGGCA ACAGAGGGTT GGTCTGCAGC
AGATGTTGGA TCGTCACCAG AGCCCACATC CAGTGAGTAT GAGCCTCCAT
TGGATGCTGT CTCCTTGGCT GAGTCTGAGC CCATGCAATA CTTTGACCCA
GATTTGGAGA CTAAGTCACA ACCAGATGAG GATAAGATGA AAGAAGACAC
CTTTGCACAC CTTACTCCAA CCCCCACCAT CTGGGTTAAT GACTCCAGTA
CATCACAGTT ATTTGAGGAT TCTACTATAG GGGAACCAGG TGTCCCAGGC
CAATCACATC TACAAGGACT GACAGACAAC ATCCACCTTG TGAAAAGTAG
TCTAAGCACT CAAGACACCT TACTGATTAA AAAGGGTATG AAAGAGATGT
CTCAGACACT ACAGGGAGGA AATATGCTAG AGGGAGACCC CACACACTCC
AGAAGTTCTG AGAGTGAGGG CCAAGAGAGC AAATCCATCA CTTTGCCTGA
CTCCACACTG GGTATAATGA GCAGTATGTC TCCAGTTAAG AAGCCTGCGG
AAACCACAGT TGGTACCCTC CTAGACAAAG ACACCACAAC AGTAACAACA
ACACCAAGGC AAAAAGTTGC TCCGTCATCC ACCATGAGCA CTCACCCTTC
TCGAAGGAGA CCCAACGGGA GAAGGAGATT ACGCCCCAAC AAATTCCGCC
ACCGGCACAA GCAAACCCCA CCCACAACTT TTGCCCCATC AGAGACTTTT
TCTACTCAAC CAACTCAAGC ACCTGACATT AAGATTTCAA GTCAAGTGGA
GAGTTCTCTG GTTCCTACAG CTTGGGTGGA TAACACAGTT AATACCCCCA
AACAGTTGGA AATGGAGAAG AATGCAGAAC CCACATCCAA GGGAACACCA
CGGAGAAAAC ACGGGAAGAG GCCAAACAAA CATCGATATA CCCCTTCTAC
AGTGAGCTCA AGAGCGTCCG GATCCAAGCC CAGCCCTTCT CCAGAAAATA
AACATAGAAA CATTGTTACT CCCAGTTCAG AAACTATACT TTTGCCTAGA
ACTGTTTCTC TGAAAACTGA GGGCCCTTAT GATTCCTTAG ATTACATGAC
AACCACCAGA AAAATATATT CATCTTACCC TAAAGTCCAA GAGACACTTC
CAGTCACATA

TAAACCCACA TCAGATGGAA AAGAAATTAA GGATGATGTT GCCACAAATG
TTGACAAACA TAAAAGTGAC ATTTTAGTCA CTGGTGAATC AATTACTAAT
GCCATACCAA CTTCTCGCTC CTTGGTCTCC ACTATGGGAG AATTTAAGGA
AGAATCCTCT CCTGTAGGCT TTCCAGGAAC TCCAACCTGG AATCCCTCAA
GGACGGCCCA GCCTGGGAGG CTACAGACAG ACATACCTGT TACCACTTCT
GGGGAAAATC TTACAGACCC TCCCCTTCTT AAAGAGCTTG AGGATGTGGA
TTTCACTTCC GAGTTTTTGT CCTCTTTGAC AGTCTCCACA CCATTTCACC
AGGAAGAAGC TGGTTCTTCC ACAACTCTCT CAAGCATAAA AGTGGAGGTG
GCTTCAAGTC AGGCAGAAAC CACCACCCTT GATCAAGATC ATCTTGAAAC
CACTGTGGCT ATTCTCCTTT CTGAAACTAG ACCACAGAAT CACACCCCTA
CTGCTGCCCG GATGAAGGAG CCAGCATCCT CGTCCCCATC CACAATTCTC
ATGTCTTTGG GACAAACCAC CACCACTAAG CCAGCACTTC CCAGTCCAAG
AATATCTCAA GCATCTAGAG ATTCCAAGGA AAATGTTTTC TTGAATTATG
TGGGGAATCC AGAAACAGAA GCAACCCCAG TCAACAATGA AGGAACACAG
CATATGTCAG GGCCAAATGA ATTATCAACA CCCTCTTCCG ACCGGGATGC
ATTTAACTTG TCTACAAAGC TGGAATTGGA AAAGCAAGTA TTTGGTAGTA
GGAGTCTACC ACGTGGCCCA GATAGCCAAC GCCAGGATGG AAGAGTTCAT
GCTTCTCATC AACTAACCAG AGTCCCTGCC AAACCCATCC TACCAACAGC
AACAGTGAGG CTACCTGAAA TGTCCACACA AAGCGCTTCC AGATACTTTG
TAACTTCCCA GTCACCTCGT CACTGGACCA ACAAACCGGA AATAACTACA
TATCCTTCTG GGGCTTTGCC AGAGAACAAA CAGTTTACAA CTCCAAGATT
ATCAAGTACA ACAATTCCTC TCCCATTGCA CATGTCCAAA CCCAGCATTC
CTAGTAAGTT TACTGACCGA AGAACTGACC AATTCAATGG TTACTCCAAA
GTGTTTGGAA ATAACAACAT CCCTGAGGCA AGAAACCCAG TTGGAAAGCC
TCCCAGTCCA AGAATTCCTC ATTATTCCAA TGGAAGACTC CCTTTCTTTA
CCAACAAGAC TCTTTCTTTT CCACAGTTGG GAGTCACCCG GAGACCCCAG
ATACCCACTT CTCCTGCCCC AGTAATGAGA GAGAGAAAAG TTATTCCAGG
TTCCTACAAC AGGATACATT CCCATAGCAC CTTCCATCTG GACTTTGGCC
CTCCGGCACC TCCGTTGTTG CACACTCCGC AGACCACGGG ATCACCCTCA
ACTAACTTAC AGAATATCCC TATGGTCTCT TCCACCCAGA GTTCTATCTC
CTTTATAACA TCTTCTGTCC AGTCCTCAGG AAGCTTCCAC CAGAGCAGCT
CAAAGTTCTT TGCAGGAGGA CCTCCTGCAT CCAAATTCTG GTCTCTTGGG
GAAAAGCCCC AAATCCTCAC CAAGTCCCCA CAGACTGTGT CCGTCACCGC
TGAGACAGAC ACTGTGTTCC CCTGTGAGGC AACAGGAAAA CCAAAGCCTT
TCGTTACTTG GACAAAGGTT TCCACAGGAG CTCTTATGAC TCCGAATACC
AGGATACAAC GGTTTGAGGT TCTCAAGAAC GGTACCTTAG TGATACGGAA
GGTTCAAGTA CAAGATCGAG GCCAGTATAT GTGCACCGCC AGCAACCTGC
ACGGCCTGGA CAGGATGGTG GTCTTGCTTT CGGTCACCGT GCAGCAACCT
CAAATCCTAG CCTCCCACTA CCAGGACGTC ACTGTCTACC TGGGAGACAC
CATTGCAATG GAGTGTCTGG CCAAAGGGAC CCCAGCCCCC CAAATTTCCT
GGATCTTCCC TGACAGGAGG GTGTGGCAAA CTGTGTCCCC

CGTGGAGAGC CGCATCACCC TGCACGAAAA CCGGACCCTT TCCATCAAGG
AGGCGTCCTT CTCAGACAGA GGCGTCTATA AGTGCGTGGC CAGCAATGCA
GCCGGGGCGG ACAGCCTGGC CATCCGCCTG CACGTGGCGG CACTGCCCCC
CGTTATCCAC CAGGAGAAGC TGGAGAACAT CTCGCTGCCC CCGGGGCTCA
GCATTCACAT TCACTGCACT GCCAAGGCTG CGCCCCTGCC CAGCGTGCGC
TGGGTGCTCG GGGACGGTAC CCAGATCCGC CCCTCGCAGT TCCTCCACGG
GAACTTGTTT GTTTTCCCCA ACGGGACGCT CTACATCCGC AACCTCGCGC
CCAAGGACAG CGGGCGCTAT GAGTGCGTGG CCGCCAACCT GGTAGGCTCC
GCGCGCAGGA CGGTGCAGCT GAACGTGCAG CGTGCAGCAG CCAACGCGCG
CATCACGGGC ACCTCCCCGC GGAGGACGGA CGTCAGGTAC GGAGGAACCC
TCAAGCTGGA CTGCAGCGCC TCGGGGGACC CCTGGCCGCG CATCCTCTGG
AGGCTGCCGT CCAAGAGGAT GATCGACGCG CTCTTCAGTT TTGATAGCAG
AATCAAGGTG TTTGCCAATG GGACCCTGGT GGTGAAATCA GTGACGGACA
AAGATGCCGG AGATTACCTG TGCGTAGCTC GAAATAAGGT TGGTGATGAC
TACGTGGTGC TCAAAGTGGA TGTGGTGATG AAACCGGCCA AGATTGAACA
CAAGGAGGAG AACGACCACA AAGTCTTCTA CGGGGGTGAC CTGAAAGTGG
ACTGTGTGGC CACCGGGCTT CCCAATCCCG AGATCTCCTG GAGCCTCCCA
GACGGGAGTC TGGTGAACTC CTTCATGCAG TCGGATGACA GCGGTGGACG
CACCAAGCGC TATGTCGTCT TCAACAATGG GACACTCTAC TTTAACGAAG
TGGGGATGAG GGAGGAAGGA GACTACACCT GCTTTGCTGA AAATCAGGTC
GGGAAGGACG AGATGAGAGT CAGAGTCAAG GTGGTGACAG CGCCCGCCAC
CATCCGGAAC AAGACTTACT TGGCGGTTCA GGTGCCCTAT GGAGACGTGG
TCACTGTAGC CTGTGAGGCC AAAGGAGAAC CCATGCCCAA GGTGACTTGG
TTGTCCCCAA CCAACAAGGT GATCCCCACC TCCTCTGAGA AGTATCAGAT
ATACCAAGAT GGCACTCTCC TTATTCAGAA AGCCCAGCGT TCTGACAGCG
GCAACTACAC CTGCCTGGTC AGGAACAGCG CGGGAGAGGA TAGGAAGACG
GTGTGGATTC ACGTCAACGT CCAGCCACCC AAGATCAACG GTAACCCCAA
CCCCATCACC ACCGTGCGGG AGATAGCAGC CGGGGGCAGT CGGAAACTGA
TTGACTGCAA AGCTGAAGGC ATCCCCACCC CGAGGGTGTT ATGGGCTTTT
CCCGAGGGTG TGGTTCTGCC AGCTCCATAC TATGGAAACC GGATCACTGT
CCATGGCAAC GGTTCCCTGG ACATCAGGAG TTTGAGGAAG AGCGACTCCG
TCCAGCTGGT ATGCATGGCA CGCAACGAGG GAGGGGAGGC GAGGTTGATC
GTGCAGCTCA CTGTCCTGGA GCCCATGGAG AAACCCATCT TCCACGACCC
GATCAGCGAG AAGATCACGG CCATGGCGGG CCACACCATC AGCCTCAACT
GCTCTGCCGC GGGGACCCCG ACACCCAGCC TGGTGTGGGT CCTTCCCAAT
GGCACCGATC TGCAGAGTGG ACAGCAGCTG CAGCGCTTCT ACCACAAGGC
TGACGGCATG CTACACATTA GCGGTCTCTC CTCGGTGGAC GCTGGGGCCT
ACCGCTGCGT GGCCCGCAAT GCCGCTGGCC ACACGGAGAG GCTGGTCTCC
CTGAAGGTGG GACTGAAGCC AGAAGCAAAC AAGCAGTATC ATAACCTGGT
CAGCATCATC AATGGTGAGA CCCTGAAGCT CCCCTGCACC CCTCCCGGGG
CTGGGCAGGG ACGTTTCTCC TGGACGCTCC CCAATGGCAT GCATCTGGAG

GGCCCCCAAA CCCTGGGACG CGTTTCTCTT CTGGACAATG GCACCCTCAC
GGTTCGTGAG GCCTCGGTGT TTGACAGGGG TACCTATGTA TGCAGGATGG
AGACGGAGTA CGGCCCTTCG GTCACCAGCA TCCCCGTGAT TGTGATCGCC
TATCCTCCCC GGATCACCAG CGAGCCCACC CCGGTCATCT ACACCCGGCC
CGGGAACACC GTGAAACTGA ACTGCATGGC TATGGGGATT CCCAAAGCTG
ACATCACGTG GGAGTTACCG GATAAGTCGC ATCTGAAGGC AGGGGTTCAG
GCTCGTCTGT ATGGAAACAG ATTTCTTCAC CCCCAGGGAT CACTGACCAT
CCAGCATGCC ACACAGAGAG ATGCCGGCTT CTACAAGTGC ATGGCAAAAA
ACATTCTCGG CAGTGACTCC AAAACAACTT ACATCCACGT CTTCTGAAAT
GTGGATTCCA GAATGATTGC TTAGGAACTG ACAACAAAGC GGGGTTTGTA
AGGGAAGCCA GGTTGGGGAA TAGGAGCTCT TAAATAATGT GTCACAGTGC
ATGGTGGCCT CTGGTGGGTT TCAAGTTGAG GTTGATCTTG ATCTACAATT
GTTGGGAAAA GGAAGCAATG CAGACACGAG AAGGAGGGCT CAGCCTTGCT
GAGACACTTT CTTTTGTGTT TACATCATGC CAGGGGCTTC ATTCAGGGTG
TCTGTGCTCT GACTGCAATT TTTCTTCTTT TGCAAATGCC ACTCGACTGC
CTTCATAAGC GTCCATAGGA TATCTGAGGA ACATTCATCA AAAATAAGCC
ATAGACATGA ACAACACCTC ACTACCCCAT TGAAGACGCA TCACCTAGTT
AACCTGCTGC AGTTTTTACA TGATAGACTT TGTTCCAGAT TGACAAGTCA
TCTTTCAGTT ATTTCCTCTG TCACTTCAAA ACTCCAGCTT GCCCAATAAG
GATTTAGAAC CAGAGTGACT GATATATATA TATATATTTT AATTCAGAGT
TACATACATA CAGCTACCAT TTTATATGAA AAAAGAAAAA CATTTCTTCC
TGGAACTCAC TTTTTATATA ATGTTTTATA TATATATTTT TTCCTTTCAA
ATCAGACGAT GAGACTAGAA GGAGAAATAC TTTCTGTCTT ATTAAAATTA
ATAAATTATT GGTCTTTACA AGACTTGGAT ACATTACAGC AGACATGGAA
ATATAATTTT AAAAAATTTC TCTCCAACCT CCTTCAAATT CAGTCACCAC
TGTTATATTA CCTTCTCCAG GAACCCTCCA GTGGGGAAGG CTGCGATATT
AGATTTCCTT GTATGCAAAG TTTTTGTTGA AAGCTGTGCT CAGAGGAGGT
GAGAGGAGAG GAAGGAGAAA ACTGCATCAT AACTTTACAG AATTGAATCT
AGAGTCTTCC CCGAAAAGCC CAGAAACTTC TCTGCAGTAT CTGGCTTGTC
CATCTGGTCT AAGGTGGCTG CTTCTTCCCC AGCCATGAGT CAGTTTGTGC
CCATGAATAA TACACGACCT GTTATTTCCA TGACTGCTTT ACTGTATTTT
TAAGGTCAAT ATACTGTACA TTTGATAATA AAATAATATT CTCCCAAAAA AAAAA

Figure 53

ATGAAGGTAAAAGGCAGAGGAATCACCTGCTTGCTGGTCTCCTTTGCTGTGATCTGCCTGGTCGCCACC
CCTGGGGGCAAGGCCTGTCCTCGCCGCTGTGCCTGTTATATGCCTACGGAGGTACACTGCACATTTCGG
TACCTGACTTCCATCCCAGACAGCATCCCGCCCAATGTGGAACGCATCAATTTAGGATACAACAGCTTG
GTTAGATTGATGGAAACAGATTTTTCTGGCCTGACCAAACTGGAGTTACTCATGCTTCACAGCAATGGC
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AAAGTCCGAAAACTTCAGAAAGATACTTTTTATGGCCTCAGGAGCTTGACACGATTGCACATGGACCAC
AACAATATTGAGTTTATAAACCCAGAGGTTTTTTATGGGCTCAACTTTCTCCGCCTGGTGCACTTGGAA
GGAAATCAGCTCACTAAGCTCCACCCAGATACATTTGTCTCTTTGAGCTACCTCCAGATATTTAAAATC
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ATGCCTGACCTAGACAGCCTTTACCTGCATGGAAACCCATGGACCTGTGATTGCCATTTAAAGTGGTTG
TCTGACTGGATACAGGAGAAGCCAGATGTAATAAAATGCAAAAAAGATAGAAGTCCCTCTAGTGCTCAG
CAGTGTCCACTTTGCATGAACCCTAGGACTTCTAAAGGCAAGCCGTTAGCTATGGTCTCAGCTGCAGCT
TTCCAGTGTGCCAAGCCAACCATTGACTCATCCCTGAAATCAAAGAGCCTGACTATTCTGGAAGACAGT
AGTTCTGCTTTCATCTCTCCCCAAGGTTTCATGGCACCCTTTGGCTCCCTCACTTTGAATATGACAGAT
CAGTCTGGAAATGAAGCTAACATGGTCTGCAGTATTCAAAAGCCCTCAAGGACATCACCCATTGCATTC
ACTGAAGAAAATGACTACATCGTGCTAAATACTTCATTTTCAACATTTTTGGTGTGCAACATAGATTAC
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CCAAGAGCAGAGATGAGGCCAGTGAAACACAAATGGACTATGATTTCAAGGGATAACAATACTAAGCTG
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Figure 54

ORIGIN

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1       MKVKGRGITC LLVSFAVICL VATPGGKACP RRCACYMPTE VHCTFRYLTS
51      IPDSIPPNVE RINLGYNSLV RLMETDFSGL TKLELLMLHS NGIHTIPDKT
101     FSDLQALQVL KMSYNKVRKL QKDTFYGLRS LTRLHMDHNN IEFINPEVFY
151     GLNFLRLVHL EGNQLTKLHP DTFVSLSYLQ IFKISFIKFL YLSDNFLTSL
201     PQEMVSYMPD LDSLYLHGNP WTCDCHLKWL SDWIQEKPDV IKCKKDRSPS
251     SAQQCPLCMN PRTSKGKPLA MVSAAAFQCA KPTIDSSLKS KSLTILEDSS
301     SAFISPQGFM APFGSLTLNM TDQSGNEANM VCSIQKPSRT SPIAFTEEND
351     YIVLNTSFST FLVCNIDYGH IQPVWQILAL YSDSPLILER SHLLSETPQL
401     YYKYKQVAPK PEDIFTNIEA DLRADPSWLM QDQISLQLNR TATTFSTLQI
451     QYSSDAQITL PRAEMRPVKH KWTMISRDNN TKLEHTVLVG GTVGLNCPGQ
501     GDPTPHVDWL LADGSKVRAP YVSEDGRILI DKSGKLELQM ADSFDTGVYH
551     CISSNYDDAD ILTYRITVVE PLVEAYQENG IHHTVFIGET LDLPCHSTGI
601     PDASISWVIP GNNVLYQSSR DKKVLNNGTL RILQVTPKDQ GYYRCVAANP
651     SGVDFLIFQV SVKMKGQRPL EHDGETEGSG LDESNPIAHL KEPPGAQLRT
701     SALMEAEVGK HTSSTSKRHN YRELTLQRRG DSTHRRFREN RRHFPPSARR
751     IDPQHWAALL EKAKKNAMPD KRENTTVSPP PVVTQLPNIP GEEDDSSGML
801     ALHEEFMVPA TKALNLPART VTADSRTISD SPMTNINYGT EFSPVVNSQI
851     LPPEEPTDFK LSTAIKTTAM SKNINPTMSS QIQGTTNQHS STVFPLLLGA
901     TEFQDSDQMG RGREHFQSRP PITVRTMIKD VNVKMLSSTT NKLLLESVNT
951     TNSHQTSVRE VSEPRHNHFY SHTTQILSTS TFPSDPHTAA HSQFPIPRNS
1001    TVNIPLFRRF GRQRKIGGRG RIISPYRTPV LRRHRYSIFR STTRGSSEKS
1051    TTAFSATVLN VTCLSCLPRE RLTTATAALS FPSAAPITFP KADIARVPSE
1101    ESTTLVQNPL LLLENKPSVE KTTPTIKYFR TEISQVTPTG AVMTYAPTSI
1151    PMEKTHKVNA SYPRVSSTNE AKRDSVITSS LSGAITKPPM TIIAITRFSR
1201    RKIPWQQNFV NNHNPKGRLR NQHKVSLQKS TAVMLPKTSP ALPQRQSSPF
1251    HFTTLSTSVM QIPSNTLTTA HHTTTKTHNP GSLPTKKELP FPPLNPMLPS
1301    IISKDSSTKS IISTQTAIPA TTPTFPASVI TYETQTERSR AQTIQREQEP
1351    QKKNRTDPNI SPDQSSGFTT PTAMTPPALA FTHSPPENTT GISSTISFHS
1401    RTLNLTDVIE ELAQASTQTL KSTIASETTL SSKSHQSTTT RKASLDTPIP
1451    PFLSSSATLM PVPISPPFTQ RAVTDTRGDS HFRLMTNTVV KLHESSRHNL
1501    QMPSSQLEPL TSSTSNLLHS TPMPALTTVK SQNSKLTPSP WAEYQFWHKP
1551    YSDIAEKGKK PEVSMLATTG LSEATTLVSD WDGQKNTKKS DFDKKPVQEA
1601    TTSKLLPFDS LSRYIFEKPR IVGGKAASFT IPANSDAFLP CEAVGNPLPT
1651    IHWTRVSGLD LSRGNQNSRV QVLPNGTLSI QRVEIQDRGQ YLCSASNLFG
1701    TDHLHVTLSV VSYPPRILER RTKEITVHSG STVELKCRAE GRPSPTVTWI
1751    LANQTVVSES SQGSRQAVVT VDGTLVLNNL SYYDRGFYKC VASNPGGQDS
1801    LLVKIQVIAA PPVILEQRRQ VIVGTWGESL KLPCTAKGTP QPSVYWVLSD
1851    GTEVKPLQFT NSKLFLFSNG TLYIRNLASS DRGTYECIAT SSTGSERRVV
1901    MLTMEERVTS PRIEAASQKR TEVNFGDKLL LNCSATGEPK PQIMWRLPSK
1951    AVVDQWSWIH VYPNGSLFIG SVTEKDSGVY LCVARNKMGD DLILMHVSLR
2001    LKPAKIDHKQ YFRKQVLHGK DFQVDCKASG SPVPEISWSL PDGTMINNAM
2051    QADDSGHRTR RYTLFNNGTL YFNKVGVAEE GDYTCYAQNT LGKDEMKVHL
2101    TVITAAPRIR QSNKTNKRIK AGDTAVLDCE VTGDPKPKIF WLLPSNDMIS
2151    FSIDRYTFHA NGSLTINKVK LLDSGEYVCV ARNPSGDDTK MYKLDVVSKP
2201    PLINGLYTNR TVIKATAVRH SKKHFDCRAE GTPSPEVMWI MPDNIFLTAP
2251    YYGSRITVHK NGTLEIRNVR LSDSADFICV ARNEGGESVL VVQLEVLEML
2301    RRPTFRNPFN EKIVAQLGKS TALNCSVDGN PPPEIIWILP NGTRFSNGPQ
2351    SYQYLIASNG SFIISKTTRE DAGKYRCAAR NKVGYIEKLV ILEIGQKPVI
2401    LTYAPGTVKG ISGESLSLHC VSDGIPKPNI KWTMPSGYVV DRPQINGKYI
2451    LHDNGTLVIK EATAYDRGNY ICKAQNSVGH TLITVPVMIV AYPPRITNRP
2501    PRSIVTRTGA AFQLHCVALG VPKPEITWEM PDHSLLSTAS KERTHGSEQL
2551    HLQGTLVIQN PQTSDSGIYK CTAKNPLGSD YAATYIQVI*
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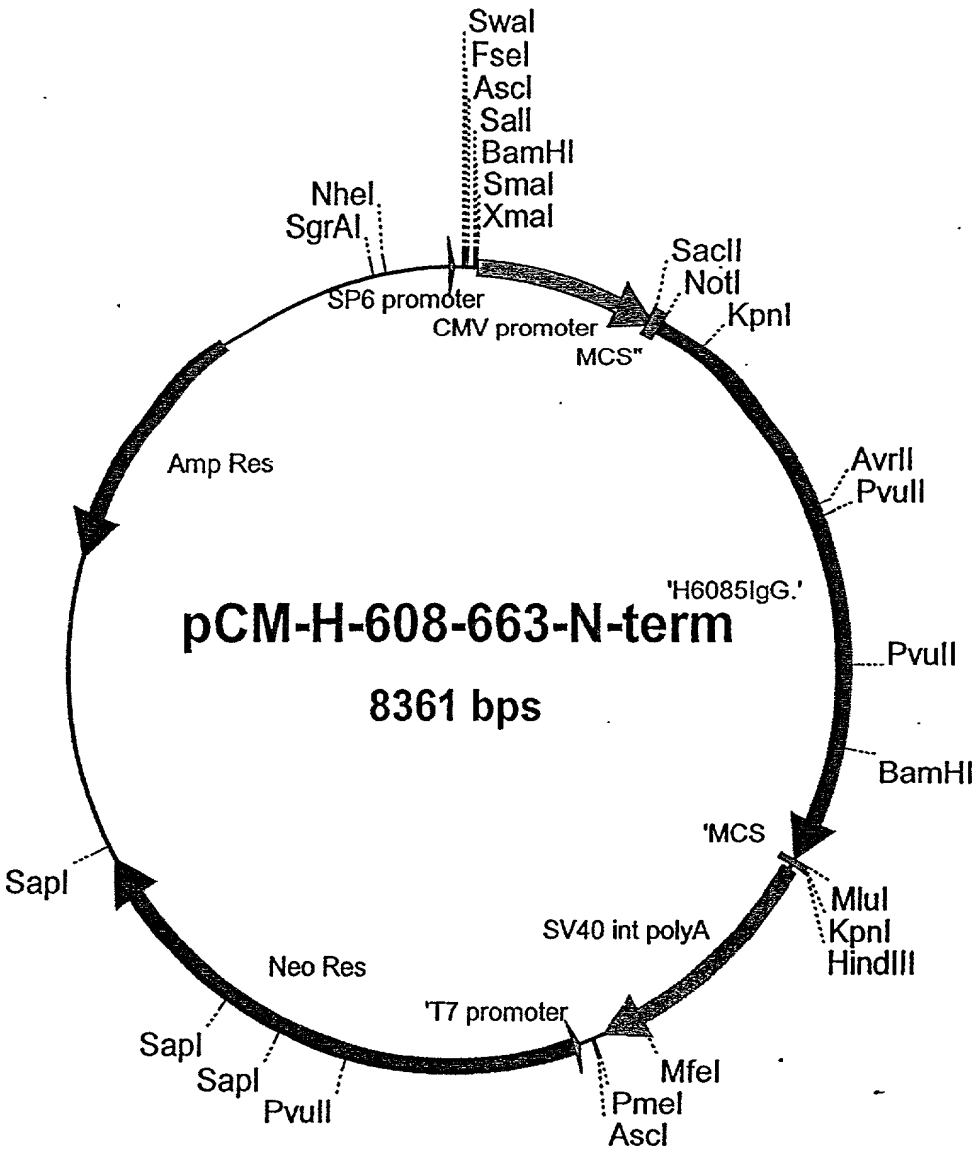
Figure 55
OCP rat amino acid sequence

>608-663Nterm Rat Protein (663 aa)

MQVRGREVSGLLISLTAVCLVVTPGSRACPRRCACYVPTEVHCTFRYLTSIPDGIPANVE
RINLGYNSLTRLTENDFDGLSKLELLMLHSNGIHRVSDKTFSGLQSLQVLKMSYNKVQII
RKDTFYGLGSLVRLHLDHNNIEFINPEAFYGLTSLRLVHLEGNRLTKLHPDTFVSLSYLQ
IFKTSFIKYLFLSDNFLTSLPKEMVSYMPNLESLYLHGNPWTCDCHLKWLSEWMQGNPDI
IKCKKDRSSSSPQQCPLCMNPRISKGRPFAMVPSGAFLCTKPTIDPSLKSKSLVTQEDNG
SASTSPQDFIEPFGSLSLNMTXXSGNKADMVCSIQKPSRTSPTAFTEENDYIMLNASFST
NLVCSVDYNHIQPVWQLLALYSDSPLILERKPQLTETPSLSSRYKQVALRPEDIFTSIEA
DVRADPFWFQQEKIVLQLNRTATTLSTLQIQFSTDAQIALPRAEMRAERLKWTMILMMNN
PKLERTVLVGGTIALSCPGKGDPSPHLEWLLADGSKVRAPYVSEDGRILIDKNGKLELQM
ADSFDAGLYHCISTNDADADVLTYRITVVEPYGESTHDSGVQHTVVTGETLDLPCLSTGV
PDASISWILPGNTVFSQPSRDRQILNNGTLRILQVTPKDQGHYQCVAANPSGADFSSFKV
SVQ

Figure 56

pCM-H-608-663-N-term



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rat                     -TSKHLPYVSLPKTLLKKPRIIGGKAASFTVPANSDVFLPCEAVGDPLPIIHWTRVSSGK
human_5+3_corrected     TTSKLLPFDSLSRYIFEKPRIVGGKAASFTIPANSDAFLPCEAVGNPLPTIHWTRVS-GL
mouse_5_corrected       ------------------------------------------------------------

rat                     KISQGTQKSRFHVLPNGTLSIQRVSIQDRGQYLCSAFNPLGVDHFHVSLSVVFYPARILD
human_5+3_corrected     DLSRGNQNSRVQVLPNGTLSIQRVEIQDRGQYLCSASNLFGTDHLHVTLSVVSYPPRILE
mouse_5_corrected       ------------------------------------------------------------

rat                     RHVKEITVHFGSTVELKCRVEGMPRPTVSWILANQTVVSETAKGSRKVWVTPDGTLIIYN
human_5+3_corrected     RRTKEITVHSGSTVELKCRAEGRPSPTVTWILANQTVVSESSQGSRQAVVTVDGTLVLHN
mouse_5_corrected       ------------------------------------------------------------

rat                     LSLYDRGFYKCVASNPSGQDSLLVKIQVITAPPVIIEQKRQAIVGVLGGSLKLPCTAKGT
human_5+3_corrected     LSIYDRGFYKCVASNPGGQDSLLVKIQVIAAPPVILEQRRQVIVGTWGESLKLPCTAKGT
mouse_5_corrected       ------------------------------------------------------------

rat                     PQPSVHWVLYDGTELKPLQLTHSRFFLYPMGTLYIRSIAPSVRGTYECIATSSSGSERRV
human_5+3_corrected     PQPSVYWVLSDGTEVKPLQFTNSKLFLFSNGTLYIRNLASSDRGTYECIATSSTGSERRV
mouse_5_corrected       ------------------------------------------------------------

rat                     VILTVEEGETIPRIETASQKWTEVNLGEKLLLNCSATGDPKPRIIWRLPSKAVIDQWHRM
human_5+3_corrected     VMLTMEERVTSPRIEAASQKRTEVNFGDKLLLNCSATGEPKPQIMWRLPSKAVVDQ----
mouse_5_corrected       ------------------------------------------------------------

rat                     GSRIHVYPNGSLVVGSVTEKDAGDYLCVARNKMGDDLVLMHVRLRLTPAKIEQKQYFKKQ
human_5+3_corrected     GSWIHVYPNGSLFIGSVTEKDSGVYLCVARNKMGDDLILMHVSLRLKPAKIDHKQYFRKQ
mouse_5_corrected       ------------------------------------------------------------

rat                     VLHGKDFQVDCKASGSPVPEVSWSLPDGTVLNNVAQADDSGYRTKRYTLFHNGTLYFNNV
human_5+3_corrected     VLHGKDFQVDCKASGSPVPEISWSLPDGTNINNAMQADDSGHRTRRYTLFNNGTLYFNKV
mouse_5_corrected       ------------------------------------------------------------

rat                     GMAEEGDYICSAQNTLGKDEMKVHLTVLTAIPRIRQSYKTTMRLRAGETAVLDCEVTGEP
human_5+3_corrected     GVAEEGDYTCYAQNTLGKDEMKVHLTVITAAPRIRQSNKTNKRIKAGDTAVLDCEVTGDP
mouse_5_corrected       ------------------------------------------------------------

rat                     KPNVFWLLPSNNVISFSNDRFTFHANRTLSIHKVKPLDSGDYVCVAQNPSGDDTKTYKLD
human_5+3_corrected     KPKIFWLLPSNDMISFSIDRYTFHANGSLTINKVKLLDSGEYVCVARNPSGDDTKMYKLD
mouse_5_corrected       ------------------------------------------------------------

rat                     IVSKPPLINGLYANKTVIKATAIRHSKKYFDCRADGIPSSQVTWIMPGNIFLPAPYFGSR
human_5+3_corrected     VVSKPPLINGLYTNRTVIKATAVRHSKKHFDCRAEGTPSPEVMWIMPDNIFLTAPYYGSR
mouse_5_corrected       ------------------------------------------------------------

rat                     VTVHPNGTLEMRNIRLSDSADFTCVVRSEGGESVLVVQLEVLEMLRRPTFRNPFNEKVIA
human_5+3_corrected     ITVHKNGTLEIRNVRLSDSADFICVARNEGGESVLVVQLEVLEMLRRPTFRNPFNEKIVA
mouse_5_corrected       ------------------------------------------------------------

rat                     QAGKPVALNCSVDGNPPPEITWILPDGTQFANRPHNSPYILMAGNGSLILYKATRNKSGKY
human_5+3_corrected     QLGKSTALNCSVDGNPPPEIIWILPNGTRFSNGPQSYQYLIASNGSFIISKTTREDAGKY
mouse_5_corrected       ------------------------------------------------------------

rat                     RCAARNKVGYIEKLILLEIGQKPVILTYRPGMVKSVSGEPLSLHCVSDGIPKPNVKWTTP
human_5+3_corrected     RCAARNKVGYIEKLVILEIGQKPVILTYAPGTVKGISGESLSLHCVSDGIPKPNIKWTMP
mouse_5_corrected       ------------------------------------------------------------
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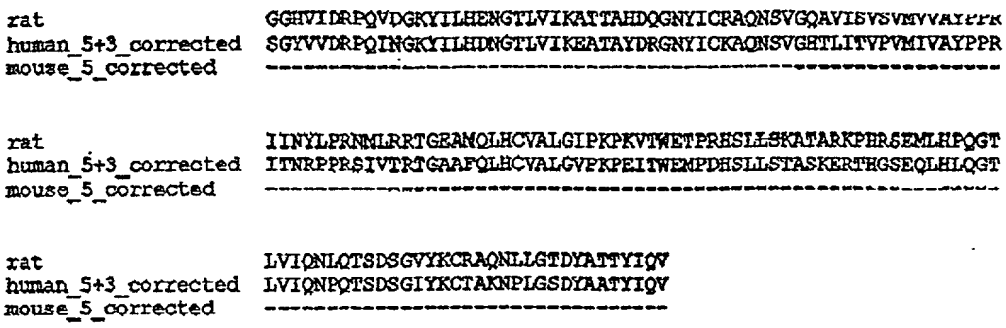

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(human_5+3_corrected: SEQ ID NO:11)
(mouse_5_corrected: SEQ ID NO:12)